

GenCore version 5.1.4-p5\_4578  
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## OM nucleic - nucleic search, using sw model

Run on: March 18, 2003, 23:07:15 ; Search time 991 Seconds

(without alignments)  
293.671 Million cell updates/sec

Title: US-09-702-498a-33-MOD

Perfect score: 10

Sequence: 1 CUUUCACCCU 10

Scoring table: IDENTITY\_NDC

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08

Maximum Match 1008

Database :

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

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2	10	100.0	6	AX477327	AX477327 Sequence
3	10	100.0	11	6 I18631	I18631 Sequence 1
4	10	100.0	12	6 AR038044	AR038044 Sequence
5	10	100.0	19	6 AR099568	AR099568 Sequence
6	10	100.0	19	6 AR178849	AR178849 Sequence
7	10	100.0	21	6 AX108449	AX108449 Sequence
8	10	100.0	21	6 AX108450	AX108450 Sequence
9	10	100.0	21	6 AX417439	AX417439 Sequence
10	10	100.0	21	6 AX476918	AX476918 Sequence
11	10	100.0	21	6 BD013048	BD013048 Paramyxov
12	10	100.0	21	6 BD013049	BD013049 Paramyxov
13	10	100.0	21	23 BD010081	BD010081 Paramyxov
14	10	100.0	21	23 BD010082	BD010082 Paramyxov
15	10	100.0	22	6 AR099567	AR099567 Sequence
16	10	100.0	22	6 AR178848	AR178848 Sequence
17	10	100.0	23	6 AR011697	AR011697 Sequence
18	10	100.0	23	6 AR092297	AR092297 Sequence
19	10	100.0	23	6 AR119514	AR119514 Sequence
20	10	100.0	23	6 AR122431	AR122431 Sequence
21	10	100.0	23	6 I33071	I33071 Sequence 7
22	10	100.0	24	6 AR099566	AR099566 Sequence
23	10	100.0	24	6 AR178847	AR178847 Sequence
24	10	100.0	47	6 BD011796	BD011796 RNP deriv
25	10	100.0	47	6 BD011797	BD011797 RNP deriv
26	10	100.0	47	23 BD004193	BD004193 RNP deriv
27	10	100.0	47	23 BD004194	BD004194 RNP deriv
28	10	100.0	53	6 A78690	A78690 Sequence 7
29	10	100.0	58	1 AF195107	AF195107 Sulfolobu
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38	10	100.0	72	23 BD004202	BD004202 RNP deriv
39	10	100.0	74	6 BD011784	BD011784 RNP deriv
40	10	100.0	74	6 BD011785	BD011785 RNP deriv
41	10	100.0	74	23 BD004181	BD004181 RNP deriv
42	10	100.0	74	23 BD004182	BD004182 RNP deriv
43	10	100.0	76	6 AX134717	AX134717 Sequence
44	10	100.0	80	6 BD011771	BD011771 RNP deriv
45	10	100.0	80	23 BD004168	BD004168 RNP deriv

## ALIGNMENTS

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RESULT 1
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LOCUS AX134713 10 bp DNA
DEFINITION Sequence 1 from Patent WO01332898.
ACCESSION AX134713
VERSION AX134713.1 GI:14271230
KEYWORDS
SOURCE
ORGANISM
synthetic construct.
artificial sequences.
REFERENCE
1 (bases 1 to 10)
AUTHORS Yonemitsu,Y., Hasegawa,M. and Alton,E.
TITLE Recombinant sendai virus vector for introducing exogenous genes to
airway epithelia
JOURNAL Patent: WO 0132898-A 1 10-MAY-2001;
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AX477327 10 bp DNA linear PAT 12-AUG-2002  
DEFINITION Sequence 1 from Patent WO0238726.  
ACCESSION AX477327  
VERSION AX477327.1 GI:22216577  
KEYWORDS  
SOURCE synthetic construct.  
ORGANISM synthetic construct.  
REFERENCE 1  
AUTHORS Griesenbach,U., Ferrari,S., Geddes,D.M., Alton,E.W., Hasegawa,M.  
and Hou,X.  
TITLE Paramyxovirus vector for gene transfer to the cardiovascular system  
JOURNML Patent: WO 0238726-A 1 16-MAY-2002;  
Dnavec Research Inc. (JP)  
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118631 11 bp DNA linear PAT 07-OCT-1996  
LOCUS 118631 Sequence 1 from patent US 5500343.  
DEFINITION 118631  
ACCESSION 118631  
VERSION 118631.1 GI:1598986  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 11)  
AUTHORS Blum,K., Noble,E.P. and Sheridan,P.J.  
TITLE Allelic association of the human dopamine(D2) receptor gene in  
compulsive disorders  
JOURNML Patent: US 5500343-A 1 19-MAR-1996;  
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AR030044/c 12 bp DNA linear PAT 29-SEP-1999  
LOCUS AR030044  
DEFINITION Sequence 233 from patent US 5861244.  
ACCESSION AR030044  
VERSION AR030044.1 GI:5943258  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 12)  
AUTHORS Wang,C.-G. and Hepburn,A.G.  
TITLE Genetic sequence assay using DNA triple strand formation  
JOURNML Patent: US 5861244-A 233 19-JAN-1999;  
FEATURES Location/Qualifiers  
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BASE COUNT 5 a 0 c 6 g 1 t  
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AR099568 19 bp DNA linear PAT 14-FEB-2001  
LOCUS AR099568  
DEFINITION Sequence 95 from patent US 6077833.  
ACCESSION AR099568  
VERSION AR099568.1 GI:12809334  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 19)  
AUTHORS Bennett,C.Frank. and Vickers,T.A.  
TITLE Oligonucleotide compositions and methods for the modulation of the  
expression of B7 protein  
JOURNML Patent: US 6077833-A 95 20-JUN-2000;  
FEATURES Location/Qualifiers  
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Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

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AR178849 19 bp DNA linear PAT 20-APR-2002  
LOCUS AR178849  
DEFINITION Sequence 95 from patent US 6315906.  
ACCESSION AR178849  
VERSION AR178849.1 GI:20219987

KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE  
AUTHORS 1 (bases 1 to 19)  
TITLE Bennett,C.Frank. and Vickers,T.A.  
JOURNAL Oligonucleotide compositions and methods for the modulation of the  
FEATURES expression of B7 protein  
Patent: US 6319906-A 95-20-NOV-2001;  
Location/Qualifiers  
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LOCUS DEFINITION Sequence 12 from Patent WO0123548.  
ACCESSION AX108449  
VERSION AX108449.1 GI:13923775  
KEYWORDS  
SOURCE synthetic construct.  
ORGANISM synthetic construct  
REFERENCE 1 (bases 1 to 21)  
AUTHORS Dorit,R.L. and Cole,K.B.  
TITLE Dna-cleaving nase p rna  
JOURNAL Patent: WO 0123548-A 12 05-APR-2001;  
YALE UNIVERSITY (US)  
Location/Qualifiers  
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Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

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RESULT 8  
AX108450 AX108450 21 bp DNA linear PAT 30-APR-2001  
LOCUS DEFINITION Sequence 13 from Patent WO0123548.  
ACCESSION AX108450  
VERSION AX108450.1 GI:13923776  
KEYWORDS  
SOURCE synthetic construct.  
ORGANISM synthetic construct  
REFERENCE 1 (bases 1 to 21)  
AUTHORS Dorit,R.L. and Cole,K.B.  
TITLE Dna-cleaving nase p rna  
JOURNAL Patent: WO 0123548-A 13 05-APR-2001;  
YALE UNIVERSITY (US)  
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AUTHORS 3 a 10 c 1 g 7 t  
TITLE  
JOURNAL  
FEATURES  
Patent: EP 1197495-A 21 17-APR-2002;  
Sumitomo Chemical Company, Limited (JP)  
Location/Qualifiers  
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Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

OY 1 CUUUCACCCU 10  
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Db 11 CTTTCACCT 2

RESULT 9  
AX417439/c AX417439 21 bp DNA linear PAT 18-JUN-2002  
LOCUS DEFINITION Sequence 21 from Patent EP1197495.  
ACCESSION AX417439  
VERSION AX417439.1 GI:21522724  
KEYWORDS  
SOURCE synthetic construct.  
ORGANISM synthetic construct  
REFERENCE 1  
AUTHORS Higashi,K. and Komatsu,K.  
TITLE Dna-binding protein yb-1-containing collagen accumulation  
JOURNAL Patent: EP 1197495-A 21 17-APR-2002;  
Sumitomo Chemical Company, Limited (JP)  
Location/Qualifiers  
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Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

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Db 11 CTTTCACCT 2

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AX476918 AX476918 21 bp DNA linear PAT 12-AUG-2002  
LOCUS DEFINITION Sequence 9 from Patent WO0220848.  
ACCESSION AX476918  
VERSION AX476918.1 GI:22216171  
KEYWORDS  
SOURCE synthetic construct.  
ORGANISM synthetic construct  
REFERENCE 1  
AUTHORS Bodnar,J.S., Castellani,L.W., Chatterjee,A., de Jong,P.,  
Lusis,A.D., Ohmen,J., Ross,D., Tafuri,S. and Wu,C.  
TITLE Gene and sequence variation associated with cancer  
JOURNAL Patent: WO 0220848-A 9 14-MAR-2002;  
THE REGENTS OF THE UNIVERSITY OF CALIFORNIA (US)  
Location/Qualifiers  
1. .21  
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/note="Synthetic Primer"  
BASE COUNT 4 a 9 c 1 g 7 t  
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Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 CUUUCACCCU 10  
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DB 11 CTTACACCT 20

RESULT 11  
BD013048 21 bp DNA linear PAT 02-AUG-2002  
LOCUS Paramyxovirus having modified transcription initiation sequence.  
DEFINITION BD013048  
ACCESSION BD013048.1 GI:22093237  
VERSION WO 0118223-A/11.  
KEYWORDS synthetic construct.  
SOURCE synthetic construct.  
ORGANISM artificial sequences.  
REFERENCE 1 (bases 1 to 21)  
AUTHORS Nagai,Y., Kato,A. and Hasegawa,M.  
TITLE Paramyxovirus having modified transcription initiation sequence  
JOURNAL Patent: WO 0118223-A 11 15-MAR-2001;  
DNAVEC RESEARCH INC, YOSHIYUKI NAGAI, ATSUSHI KATO, MAMORU HASEGAWA  
COMMENT OS Artificial Sequence  
PN WO 0118223-A/11  
PD 15-MAR-2001  
PF 06-SEP-2000 WO 2000JP06051  
PR 06-SEP-1999 JP 99P 252231  
PI YOSHIYUKI NAGAI, ATSUSHI KATO, MAMORU HASEGAWA  
PC C12N15/86, C12N15/45//A61K31/7105, A61K48/00  
CC Description of Artificial Sequence: artificially synthesized primer  
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Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

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DEFINITION BD013049  
ACCESSION BD013049.1 GI:22093238  
VERSION WO 0118223-A/12.  
KEYWORDS synthetic construct.  
SOURCE synthetic construct.  
ORGANISM artificial sequences.  
REFERENCE 1 (bases 1 to 21)  
AUTHORS Nagai,Y., Kato,A. and Hasegawa,M.  
TITLE Paramyxovirus having modified transcription initiation sequence  
JOURNAL Patent: WO 0118223-A 12 15-MAR-2001;  
DNAVEC RESEARCH INC, YOSHIYUKI NAGAI, ATSUSHI KATO, MAMORU HASEGAWA  
COMMENT OS Artificial Sequence  
PN WO 0118223-A/12  
PD 15-MAR-2001  
PF 06-SEP-2000 WO 2000JP06051  
PR 06-SEP-1999 JP 99P 252231  
PI YOSHIYUKI NAGAI, ATSUSHI KATO, MAMORU HASEGAWA

PC C12N15/86, C12N15/45//A61K31/7105, A61K48/00  
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DB 9 CTTACACCT 18

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DT 08-FEB-2002 (Rel. 70, Created)  
DT 08-FEB-2002 (Rel. 70, Last updated, Version 1)  
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DE Paramyxovirus having modified transcription initiation sequence.  
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KW JP 03075813-T/11.  
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OS synthetic construct  
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RP 1-21  
RA Nagai Y., Kato A., Hasegawa M.;  
RT "Paramyxovirus having modified transcription initiation sequence";  
RL Patent number JP03075813-T/11, 06-MAR-2001.  
RL DNAVEC RESEARCH INC, YOSHIYUKI NAGAI, ATSUSHI KATO, MAMORU HASEGAWA.  
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CC CC PD 06-MAR-2001  
CC PF 06-SEP-2000 JP 2000006051  
CC PR 06-SEP-1999 JP 99P 252231  
CC PI YOSHIYUKI NAGAI, ATSUSHI KATO, MAMORU HASEGAWA  
CC C12N15/86, C12N15/45//A61K31/7105, A61K48/00  
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Query Match 100.0%; Score 10; DB 23; Length 21;  
Best Local Similarity 60.0%; Pred. No. 1.9e+05;  
Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 CUUUCACCCU 10  
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Db 13 CTTTCACCCCT 4

RESULT 14

ID BD010082 standard; DNA; SYN; 21 BP.

AC BD010082;

SV BD010082.1

XX 08-FEB-2002 (Rel. 70, Created)

DT 08-FEB-2002 (Rel. 70, Last updated, Version 1)

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DE Paramyxovirus having modified transcription initiation sequence.

XX JP 03075813-T/12.

XX

XX synthetic construct

OC artificial sequence.

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RA Nagai Y., Kato A., Hasegawa M.;

RT "Paramyxovirus having modified transcription initiation sequence";

RL Patent number JP03075813-T/12, 06-MAR-2001.

RL DNAVEC RESEARCH INC, YOSHITUKI NAGAI, ATSUSHI KATO, MAMORU HASEGAWA.

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CC OS Artificial Sequence

CC PN JP 03075813-T/12

CC PD 06-MAR-2001

CC PF 06-SEP-2000 JP 2000006051

CC PR 06-SEP-1999 JP -99 252231

CC PI YOSHITUKI NAGAI, ATSUSHI KATO, MAMORU HASEGAWA

CC PC C12N15/86, C12N15/45//A61K31/7105, A61K48/00

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CC FH Key

CC FT source

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CC FT Location/Qualifiers

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Query Match 100.0%; Score 10; DB 23; Length 21;

Best Local Similarity 60.0%; Pred. No. 1.9e+05;

Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

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Db 9 CTTTCACCCCT 18

RESULT 15

AR099567

LOCUS AR099567 22 bp DNA linear PAT 14-FEB-2001

DEFINITION Sequence 94 from patent US 6077833.

ACCESSION AR099567

VERSION AR099567.1 GI:12809333

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 22)

AUTHORS Bennett, C. Frank. and Vickers, T. A.

TITLE Oligonucleotide compositions and methods for the modulation of the expression of B7 protein

JOURNAL Patent: US 6077833-A 94 20-JUN-2000;

FEATURES Location/Qualifiers

source 1. .22

BASE COUNT 6 a 6 c 5 g 5 t

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Db 10 CTTTCACCCCT 19

Search completed: March 19, 2003, 00:40:37

Job time : 991 secs

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GenCore version 5.1.4\_p5-4578  
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OM nucleic - nucleic search, using sw model

Run on: March 18, 2003, 23:06:05 ; Search time 168 Seconds

(without alignments)  
134,048 Million cell updates/sec

Title: US-09-702-498A-33-MOD

Sequence: 10  
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Searched: 2185239 seqs, 112599159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

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- 7: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1986.DAT:\*
- 8: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1987.DAT:\*
- 9: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1988.DAT:\*
- 10: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1989.DAT:\*
- 11: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1990.DAT:\*
- 12: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1991.DAT:\*
- 13: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1992.DAT:\*
- 14: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT:\*
- 15: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1994.DAT:\*
- 16: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1995.DAT:\*
- 17: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1996.DAT:\*
- 18: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1997.DAT:\*
- 19: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT:\*
- 20: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT:\*
- 21: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT:\*
- 22: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:\*
- 23: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:\*
- 24: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	10	100.0	10	22	AA165896
2	10	100.0	10	22	AAH73613
3	10	100.0	10	22	AAH23653
4	10	100.0	10	22	AAH6115
5	10	100.0	10	22	AAH77598
6	10	100.0	10	24	AAH47265
7	10	100.0	10	24	AAH38107
8	10	100.0	10	24	ABK48812
9	10	100.0	10	24	ABH39904

C	10	10	100.0	11	15	AA057929	Oligonucleotide #1
C	11	10	100.0	11	17	AAH18122	Human dopamine D2
C	12	10	100.0	12	20	AAH14846	Triple helix form1
C	13	10	100.0	13	23	ABP08726	Oligonucleotide SE
C	14	10	100.0	13	23	ABP08727	Oligonucleotide SE
C	15	10	100.0	13	23	ABH24716	Oligonucleotide SE
C	16	10	100.0	13	23	ABH24717	Oligonucleotide SE
C	17	10	100.0	14	22	AAH77602	Modified transcript
C	18	10	100.0	14	22	AAH77603	Modified transcript
C	19	10	100.0	14	22	AAH77605	Modified transcript
C	20	10	100.0	15	22	AAH70291	Human DRD2 allele
C	21	10	100.0	15	22	AAH70299	Human DRD2 allele
C	22	10	100.0	15	22	AAH70389	Human DRD2 allele
C	23	10	100.0	15	22	AAH70391	Human DRD2 allele
C	24	10	100.0	17	24	ABK56874	Human C1CA1 gene e
C	25	10	100.0	17	24	ABK57095	Human C1CA1 gene e
C	26	10	100.0	17	24	ABK57570	Human C1CA1 gene e
C	27	10	100.0	17	24	ABK57571	Human C1CA1 gene e
C	28	10	100.0	19	19	AAH48056	Human B7-2 target
C	29	10	100.0	19	19	AAH48056	Human B7-2 target
C	30	10	100.0	21	22	AAH86495	Human B7-2 target
C	31	10	100.0	21	22	AAH86495	Human B7-2 target
C	32	10	100.0	21	22	AAH86496	Human B7-2 target
C	33	10	100.0	21	22	AAH77591	Modified transcript
C	34	10	100.0	21	22	AAH77592	Modified transcript
C	35	10	100.0	21	22	AAH77590	Human gene single
C	36	10	100.0	21	24	ABK50521	PCR primer #1 for
C	37	10	100.0	21	24	ABK70908	Human familial com
C	38	10	100.0	22	19	ABK68004	Human FCRL1 locus
C	39	10	100.0	22	22	AAH48055	Human B7-2 target
C	40	10	100.0	23	15	AAH3897	Human B7-2 target
C	41	10	100.0	23	15	AAH3898	Human B7-2 target
C	42	10	100.0	23	19	AAH23970	Angiotensinogen mo
C	43	10	100.0	23	21	AAH23970	PCR primer for detecti
C	44	10	100.0	23	21	AAH23970	PCR primer used to
C	45	10	100.0	24	22	AAH67107	Human angiotensino
						AAH70469	Human DRD2 exon 6

#### ALIGNMENTS

AA165896	RESULT 1
ID	AA165896 standard; DNA; 10 BP.
AC	AA165896;
XX	
XX	
XX	
DT	03-JAN-2002 (first entry)
XX	
XX	
DE	Nucleotide sequence of a synthetic oligonucleotide.
XX	
KW	Vaccine; Sendai virus vector; viral protein; immunodeficiency virus;
KW	AIDS; antigen gene; nasal mucosa; lymph node; ss.
XX	
OS	Synthetic.
XX	
PN	WO200172340-A1.
XX	
PD	04-OCT-2001.
XX	
PF	30-MAR-2001; 2001WO-JP02769.
XX	
PR	30-MAR-2000; 2000US-193127P.
XX	
PA	(DNAV-) DNAVEC RES INC.
PA	(NINA) JAPAN NAT INST INFECTIOUS DISEASES.
XX	
PI	Kano M, Matano T, Kato A, Nagai Y, Hasegawa M;
XX	
DR	WPI; 2001-616443/71.
XX	
PT	Viral protein of immunodeficiency virus-encoding Sendai virus
PT	vector-based AIDS virus vaccine for provision of efficient protective

PT Immunity comprises nasal administration to e.g. macaque to suppress  
PT onset and progress of AIDS  
XX  
XX  
PS Disclosure: Page 27, 92pp; Japanese.  
CC The specification describes a vaccine containing a Sendai virus vector  
CC which encodes the viral protein of immunodeficiency virus. The vaccine  
CC is for treating AIDS, with expression of antigen gene mediated by the  
CC vector in nasal mucosa and local lymph nodes detected and  
CC antigen-specific cell-mediated response induced at significant  
CC level after vaccination. The present sequence represents an  
CC oligonucleotide which is used in the course of the invention.  
XX  
SQ Sequence 10 BP; 1 A; 5 C; 0 G; 4 T; 0 other;  
  
Query Match 100.0%; Score 10; DB 22; Length 10;  
Best Local Similarity 60.0%; Pred. No. 4.2e+03;  
Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 CUUUCACCCU 10  
1:::|||||  
DB 1 CTTTCACCCCT 10  
  
RESULT 2  
AAH73613  
ID AAH73613 standard; DNA; 10 BP.  
XX  
XX AAH73613;  
AC  
XX  
DT 27-SEP-2001 (first entry)  
XX  
XX DNA sequence, SEQ ID NO: 1.  
DE  
XX  
XX Gene therapy; vascular disorder; recombinant paramyxovirus vector; ds.  
KW  
XX  
XX Unidentified.  
OS  
XX WO200153491-A1.  
XX  
XX 26-JUL-2001.  
XX  
XX 11-JAN-2001; 2001WO-JP00087.  
XX  
XX 19-JAN-2000; 2000JP-0014136.  
XX  
XX (DNAV-) DNAVEC RES INC.  
XX  
XX Masaki I, Yonemitsu Y, Suelshi K, Hasegawa M, Kinoh H;  
XX WPI; 2001-457610/49.  
DR  
XX  
XX Paramyxovirus vector containing foreign gene for efficient gene  
PT transfer into vascular cells  
PT  
XX  
XX Disclosure: Page 19; 84pp; Japanese.  
PS  
XX  
XX The invention relates to a method for inserting nucleic acid into blood  
CC vessel cells by contacting the cells with the nucleic acid contained in a  
CC recombinant paramyxovirus vector or cells transformed by it. The  
CC method can be used for gene therapy of vascular disorders. Genes that  
CC can be introduced into blood vessel cells by this method include cell  
CC cycle regulators (such as p53, p21, p16 and p27), inhibitory factors  
CC (such as H-Ras, enos and C-natriuretic peptide), ion channels (such as  
CC Kir 6.2 potassium channel), blood proteins (such as urokinase and  
CC tissue plasminogen activator), tissue factor pathway inhibitors (such  
CC as TFPI) and vascular growth factors (such as vascular endothelial  
CC growth factor (VEGF), fibroblast growth factor (FGF) and hepatocyte  
CC growth factor (HGF)). The present sequence is provided in the  
CC specification.  
XX  
SQ Sequence 10 BP; 1 A; 5 C; 0 G; 4 T; 0 other;

Query Match 100.0%; Score 10; DB 22; Length 10;  
Best Local Similarity 60.0%; Pred. No. 4.2e+03;  
Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 CUUUCACCCU 10  
1:::|||||  
DB 1 CTTTCACCCCT 10  
  
RESULT 3  
AAH23653  
ID AAH23653 standard; DNA; 10 BP.  
XX  
XX AAH23653;  
AC  
XX  
XX 07-AUG-2001 (first entry)  
DT  
XX  
XX S. sequence oligonucleotide used in a recombinant Sendai virus vector.  
DE  
XX  
XX Gene therapy; S sequence; airway epithelium; cystic fibrosis; ds.  
KW  
XX  
XX Parainfluenza virus.  
OS  
XX  
XX WO200132898-A2.  
XX  
XX 10-MAY-2001.  
PD  
XX  
XX 02-NOV-2000; 2000WO-JP07737.  
PF  
XX  
XX 02-NOV-1999; 99US-0163055.  
PR  
XX 17-DEC-1999; 99JP-0359218.  
XX  
XX (DNAV-) DNAVEC RES INC.  
XX  
XX Yonemitsu Y, Hasegawa M, Alton EW;  
XX WPI; 2001-328799/34.  
DR  
XX  
XX New chorioallantoic fluid containing a recombinant Sendai virus vector  
PT carrying an exogenous gene, useful in gene therapy, particularly for  
PT treating cystic fibrosis in mammals, e.g. human, mouse, rabbit, sheep,  
PT bovine or monkey  
PT  
XX  
XX Disclosure: Page 7; 42pp; English.  
PS  
XX  
XX The present invention relates to a composition for introducing exogenous  
CC genes to airway epithelia. The composition comprises a recombinant Sendai  
CC virus vector carrying an exogenous gene. The composition is useful in  
CC gene therapy. In particular, the composition is useful for treating  
CC cystic fibrosis in mammals, e.g. human, mouse, rabbit, sheep, bovine or  
CC monkey. The present sequence was used in the composition of the present  
CC invention as a transcription start sequence.  
XX  
SQ Sequence 10 BP; 1 A; 5 C; 0 G; 4 T; 0 other;  
  
Query Match 100.0%; Score 10; DB 22; Length 10;  
Best Local Similarity 60.0%; Pred. No. 4.2e+03;  
Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 CUUUCACCCU 10  
1:::|||||  
DB 1 CTTTCACCCCT 10  
  
RESULT 4  
AAF86115  
ID AAF86115 standard; DNA; 10 BP.  
XX  
XX AAF86115;  
AC  
XX  
XX 21-JUN-2001 (first entry)  
DT  
XX  
XX Sendai virus S sequence oligonucleotide.



XX Extracellular superoxide dismutase; EC-SOD; immunosuppressive;  
 KW antiinflammatory; antiarthritis; antirheumatic; arthritis; colitis;  
 KW systemic autoimmune disease; systemic lupus erythematosus;  
 KW rheumatic myocarditis; progressive systemic sclerosis; dermatomyositis;  
 KW Sjogren's syndrome; polyarteritis; Sendai virus; ss.  
 OS Parainfluenza virus.  
 XX CA2316518-A1.  
 XX 01-MAR-2001.  
 XX 31-AUG-2000; 2000CA-2316518.  
 XX 01-SEP-1999; 99JP-0248032.  
 PR 27-APR-2000; 2000CA-2304453.  
 XX (DNAV-) DNA VEC RES INC.  
 PA Yamauchi N, Fukumura M, Iyama S, Hasegawa M, Nitsui Y;  
 PI WPI; 2001-300717/32.  
 DR New EC-SOD proteins and nucleic acids encoding the protein useful in  
 PT gene therapy for treating or preventing systemic autoimmune diseases,  
 PT e.g. rheumatoid arthritis, colitis and systemic lupus erythematosus -  
 XX disclosure; Page 24; 71pp; English.  
 XX This invention relates to a superoxide dismutase (SOD) protein which  
 CC exists extracellularly and is termed EC-SOD, and the polynucleotide  
 CC encoding it. SOD is the enzyme that catalyses the reaction involved in  
 CC superoxide anion radical production. The invention includes a vector  
 CC containing the EC-SOD coding sequence, and a method for treating or  
 CC preventing systemic autoimmune diseases comprising administering the  
 CC vector. Methods using the EC-SOD protein and DNA sequences result in  
 CC immunosuppressive, anti-inflammatory, antiarthritis, and antirheumatic  
 CC activity. The EC-SOD protein and nucleic acid encoding the protein are  
 CC useful for treating systemic autoimmune diseases such as arthritis,  
 CC rheumatoid arthritis, colitis, systemic lupus erythematosus, rheumatic  
 CC myocarditis, progressive systemic sclerosis,  
 CC dermatomyositis/polyomyositis, mixed connective tissue disease, Sjogren's  
 CC syndrome, polyarteritis, Wegener granulomatosis and colitis. The present  
 CC sequence represents a Sendai virus (Parainfluenza virus) oligonucleotide  
 CC which can be used in the construction of a vector containing the EC-SOD  
 CC gene.  
 XX Sequence 10 BP; 1 A; 5 C; 0 G; 4 T; 0 other;  
 SO  
 XX Query Match 100.0%; Score 10; DB 22; Length 10;  
 XX Best Local Similarity 60.0%; Pred. No. 4.2e+03;  
 XX Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;  
 OY 1 CUUUCACCCU 10  
 Db 1 CTTTCACCTT 10  
 1:::|||||:  
 1 CTTTCACCTT 10  
 RESULT 5  
 AAF77598  
 ID AAF77598 standard; DNA; 10 BP.  
 XX AAF77598;  
 AC  
 XX 29-MAY-2001 (first entry)  
 DT Modified transcription initiation site Paramyxovirus related oligo #18.  
 DE Transcription initiation sequence; viral vector; vaccine; therapy; ds.  
 KW Unidentified.  
 OS  
 XX

PN WO200118223-A1.  
 XX 15-MAR-2001.  
 PD 06-SEP-2000; 2000MO-JP06051.  
 XX 06-SEP-1999; 99JP-0252231.  
 PR (DNAV-) DNAVEC RES INC.  
 PA Nagai Y, Kato A, Hasegawa M;  
 PI WPI; 2001-244576/25.  
 DR Paramyxovirus vectors with modified transcription initiation sequences  
 XX for increased expression of foreign genes in production of drugs and  
 PT vaccines -  
 PS disclosure; Page 17; 65pp; Japanese.  
 XX The present invention describes a paramyxovirus vector DNA in which the  
 CC transcription initiation sequence has been modified to modify the  
 CC expression of a gene located downstream of the transcription initiation  
 CC sequence. This is useful in the production of mutant paramyxovirus  
 CC vectors with elevated gene expression and a more rapid proliferation than  
 CC the wild-type vector, which can then be used for more efficient  
 CC production of drug substances and vaccines.  
 XX Sequence 10 BP; 1 A; 5 C; 0 G; 4 T; 0 other;  
 SO  
 XX Query Match 100.0%; Score 10; DB 22; Length 10;  
 XX Best Local Similarity 60.0%; Pred. No. 4.2e+03;  
 XX Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;  
 OY 1 CUUUCACCCU 10  
 Db 1 CTTTCACCTT 10  
 1:::|||||:  
 1 CTTTCACCTT 10  
 RESULT 6  
 AAL47265  
 ID AAL47265 standard; DNA; 10 BP.  
 XX AAL47265;  
 AC  
 XX 30-AUG-2002 (first entry)  
 DT Sendai virus S sequence complement.  
 XX Sendai virus S sequence complement.  
 DE Sendai virus vector; gene therapy; antiinflammatory; inflammation;  
 KW cardiovascular system; paramyxovirus; IL-10; pulmonary fibrosis;  
 KW sclerosing peritonitis; prostatomegaly; multiple sclerosis;  
 KW neuoprotective; immunosuppressive; antidiabetic; antirheumatic;  
 KW transplant rejection; diabetes; chronic articular rheumatism;  
 KW psoriasis; inflammatory enteropathy; systemic lupus erythematosus;  
 KW iritis; granulomatous disease; chronic nephritis; scleroderma;  
 KW hysteriomyoma; keloid; cirrhosis; cystic fibrosis; pneumonia; ss.  
 XX Sendai virus.  
 OS  
 XX WO200238726-A2.  
 PN 16-MAY-2002.  
 PD 08-NOV-2001; 2001WO-JP09786.  
 PF 08-NOV-2000; 2000JP-0339942.  
 PR (DNAV-) DNAVEC RES INC.  
 PA Griesenbach U, Ferrari S, Geddes DM, Alton EW, Hasegawa M, Hou X;  
 PI WPI; 2002-490069/52.  
 DR

XX Novel paramyxovirus vector for gene transfer to cardiovascular system,  
PT in which expression product of gene comprised in vector is transferred  
PT to a site different from the site of administration through the  
PS bloodstream  
PS Disclosure; Page 17; 67pp; English.

XX The present invention relates to a paramyxovirus vector for gene transfer  
CC to the cardiovascular system, where the expression product of a gene  
CC comprised in the vector is transferred to a site different from the site  
CC of administration through the bloodstream. The vector is useful for  
CC transferring sequences such as IL-10 to the cardiovascular system, for  
CC treating pneumonia in cystic fibrosis patients and for treating  
CC inflammatory diseases such as pulmonary fibrosis, sclerosing peritonitis,  
CC prostatically, multiple sclerosis, post transplant rejection, diabetes,  
CC chronic articular rheumatism, psoriasis, inflammatory enteropathy,  
CC systemic lupus erythematosus, iritis, granulomatous disease, chronic  
CC nephritis, scleroderma, lymphoma, keloid and cirrhosis. The present  
CC sequence is a DNA fragment used to produce the vector of the invention.

XX Sequence 10 BP; 1 A; 5 C; 0 G; 4 T; 0 other;

QY Query Match 100.0%; Score 10; DB 24; Length 10;  
Best Local Similarity 60.0%; Pred. No. 4.2e+03;  
Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 CUUUCACCCU 10  
1 CTTTCACCCCT 10

Db 1 CTTTCACCCCT 10

RESULT 7  
AAL38107  
ID AAL38107 standard; DNA; 10 BP.  
XX AAL38107;  
XX AAL38107;  
DT 15-AUG-2002 (first entry)

XX Angiogenesis gene containing paramyxovirus vector related oligo #1.  
DE Vasotrophic; paramyxovirus vector; angiogenesis gene; gene therapy; FGF2;  
KM ischaemia; virus vector; edema; tissue targeting; ds.  
XX Unidentified.  
OS WO200242481-A1.  
XX 30-MAY-2002.  
XX 27-NOV-2001; 2001WO-JP10323.  
XX 27-NOV-2000; 2000JP-0359374.  
XX (DNAV-) DNAVEC RES INC.  
XX Yonemitsu Y, Sueishi K, Fukumura M, Hou X, Hasegawa M;  
XX WPI; 2002-452662/48.  
XX Paramyxovirus vector containing angiogenesis gene FGF2 for gene therapy  
PT treatment targeting ischemic tissue  
XX Disclosure; Page 23; 94pp; Japanese.

XX The invention relates to a paramyxovirus vector containing an  
CC angiogenesis gene, which can be used for gene therapy of ischaemia in  
CC tissues including brain, heart, lung, skeletal muscle and kidney. The  
CC expression of the virus vector is free from edema and specific tissues  
CC can be targeted. This polynucleotide sequence represents an artificial  
CC oligonucleotide relating to the paramyxovirus vector containing an  
CC angiogenesis gene FGF2 of the invention.

XX Sequence 10 BP; 1 A; 5 C; 0 G; 4 T; 0 other;

QY Query Match 100.0%; Score 10; DB 24; Length 10;  
Best Local Similarity 60.0%; Pred. No. 4.2e+03;  
Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 CUUUCACCCU 10  
1 CTTTCACCCCT 10

Db 1 CTTTCACCCCT 10

RESULT 8  
ABK48812  
ID ABK48812 standard; DNA; 10 BP.  
XX ABK48812;  
XX ABK48812;  
DT 15-JUL-2002 (first entry)

XX DNA sequence #1 relating to paramyxovirus vector for gene transfer.

XX Method for gene transfer; skeletal muscle; paramyxovirus vector;  
KM gene therapy; neuromuscular disorder; tumourigenesis; neuroprotective;  
KM myotrophic; insulin-like growth factor; IGF; ds.  
XX Unidentified.  
OS WO200231138-A1.  
XX 18-APR-2002.  
XX 26-SEP-2001; 2001WO-JP08372.  
XX 06-OCT-2000; 2000JP-0308533.  
XX (DNAV-) DNAVEC RES INC.  
XX Hukumura M, Shiota A, Maeda M, Hasegawa M;  
XX WPI; 2002-340180/37.  
XX Paramyxovirus vector for transferring foreign gene e.g. insulin-like  
PT growth factor into skeletal muscle in gene therapy of neuromuscular  
PT disorders  
XX Disclosure; Page 14; 56pp; Japanese.

XX The present invention relates to a method for transferring a foreign  
CC gene into skeletal muscle. The method comprises administering a  
CC paramyxovirus inserted with the foreign gene. The paramyxovirus vector  
CC is useful for transferring a foreign gene e.g. insulin-like growth  
CC factor (IGF) into skeletal muscle in the gene therapy of neuromuscular  
CC disorders. Such a vector can sustain transgene expression for up to a  
CC month after injection and is safe, non-infective and does not cause  
CC tumourigenesis. The present DNA sequence of unknown function is  
CC given in the specification of the present invention.

XX Sequence 10 BP; 1 A; 5 C; 0 G; 4 T; 0 other;

QY Query Match 100.0%; Score 10; DB 24; Length 10;  
Best Local Similarity 60.0%; Pred. No. 4.2e+03;  
Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 CUUUCACCCU 10  
1 CTTTCACCCCT 10

Db 1 CTTTCACCCCT 10

RESULT 9  
ABL39904  
ID ABL39904 standard; DNA; 10 BP.  
XX

AC		ABLJ3904;
XX		
DT		14-MAY-2002 (first entry)
XX		
DE		Sendai virus S oligonucleotide SEQ ID NO:1.
XX		
KW		Sendai virus; Sendai virus vector; renal cell; paramyxovirus; gene transfer;
KM		gene therapy; kidney; nephrotropic; antidiabetic; diabetes; renopathy;
KW		chronic glomerulonephritis; glomerulosclerosis; Alport's syndrome;
KM		tubulointerstitial nephritis; ss.
XX		
OS		Parainfluenza virus.
XX		
PX		WO200200264-A1.
PN		
PD		03-JAN-2002.
XX		
PF		27-JUN-2001; 2001MO-JP05513.
XX		
PR		27-JUN-2000; 2000JP-0197870.
PA		(DNAV-) DNAVEC RES INC.
PI		
DR		Imai E, Isaka Y, Fukumura M, Hasegawa M;
XX		WPI; 2002-130841/17.
PT		
PT		Transferring a gene into renal cells, useful for gene therapy of a
PT		kidney to treat e.g. chronic glomerulonephritis, comprises using a
PS		virus vector particularly of paramyxovirus -
XX		
XX		Example 1; Page 38; 75pp; Japanese.
CC		
CC		The present invention describes transferring a gene into renal cells
CC		comprising contacting a paramyxovirus vector with the renal cells,
CC		particularly by administration into blood vessels, especially the renal
CC		artery or into the urethra. Also described are: (1) a paramyxovirus
CC		vector for use in transferring a gene into renal cells; and
CC		(2) compositions for transferring a gene into renal cells comprising
CC		cells having the paramyxovirus vector or the vector. The method is used
CC		for transferring a gene into renal cells. The virus is applicable in
CC		gene therapy for the kidney to treat target diseases of e.g. chronic
CC		glomerulonephritis, diabetes, renopathy, glomerulosclerosis,
CC		tubulointerstitial nephritis and Alport's syndrome. The transfer of a
CC		gene into renal cells is with high efficiency, and after brief exposure,
CC		the transferred gene is continuously expressed in renal cells over a
CC		long period of time. The present sequence represents a Sendai virus
CC		(parainfluenza virus) oligonucleotide which is used in an example from
CC		the present invention.
XX		
SC		Sequence 10 BP; 1 A; 5 C; 0 G; 4 T; 0 other;
		Query Match                      100.0%; Score 10; DB 24; Length 10;
		Best Local Similarity    60.0%; Pred. No. 4, 2e+03;
		Matches    6; Conservative         4; Mismatches    0; Indels         0; Gaps         0;
OY		- 1 CUUUCACCCU 10
		:::     :
DB		1 CTTTCACCGT 10
RESULT 10		
ID		AAO57929/c
XX		AAO57929 standard; DNA: 11 BP.
XX		
AC		AAO57929;
XX		
DT		12-AUG-1994 (first entry)
XX		
DE		Oligonucleotide #1 to diagnose compulsive behaviour disorders.
XX		
KW		Human dopamine D2 receptor; genetic susceptibility; diagnosis;
KM		DNR2; compulsive disorder; alcoholism; cocaine dependence;

KW	Tourette's Syndrome; attention deficit disorder; hyperactivity;
KW	post-traumatic stress disorder; PCR amplification; RFLP;
KW	restriction fragment length polymorphism; ss.
OS	Synthetic.
PN	AU9331129-A.
XX	
PD	06-JAN-1994.
XX	
PF	11-JAN-1993; 93AU-0031129.
XX	
PR	24-JUN-1992; 92US-0909282.
XX	
PA	(REGC ) UNIV CALIFORNIA.
PA	(TEXA ) UNIV TEXAS SYSTEM.
PI	
PI	Blum K, Noble EP, Sheridan PJ;
DR	WPI; 1994-057631/08.
XX	
PT	Detecting a genetic potential susceptibility to a compulsive
PT	disorder - by detecting in DNA from a subject a human dopamine D2
PT	receptor gene allele
XX	
PS	Disclosure: Page 148; 165pp; English.
XX	
CC	Compulsive disorder susceptibility in humans can be detected
CC	by determining the presence or absence of a particular dopamine D2
CC	receptor allele in a DNA sample. Partic. the A1 and B1 alleles are
CC	detected, as these alleles have been found to be present in a
CC	majority of clinically diagnosed alcoholics and cocaine users.
CC	Detection can be by PCR amplification (see AAQ57927-8 for pref.
CC	primers) or by restriction fragment length polymorphism.
CC	(N.B. There are no direct references to AAQ57929-Q57932 in the
CC	specification.)
XX	
SQ	Sequence 11 BP; 4 A; 0 C; 6 G; 1 T; 0 other;
	Query Match 100.0%; Score 10; DB 15; Length 11;
	Best Local Similarity 60.0%; Pred. No. 4, 3e+03;
	Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
OY	1 CUUUCACCCU 10 1:::     :
DB	11 CTTTCACCCT 2
RESULT 11	
AAAT18122/c	
ID	AAAT18122 standard; DNA: 11 BP.
XX	
XX	AAAT18122;
AC	
XX	
DT	22-AUG-1996 (first entry)
XX	
DE	Human dopamine D2 receptor DRD2 intron 6 polymorphic site (3208T).
XX	
RW	Dopamine D2 receptor; A1 allele; B1 allele; polymerase chain reaction;
KW	PCR amplification of specific alleles; PNAS; compulsive disorder;
XX	cocaine dependence; alcoholism; genetic susceptibility; ss.
XX	
OS	Homo sapiens.
XX	
FH	Key
FT	allele
FT	Location/Qualifiers
FT	6
FT	/tag-
FT	- "nucleotides 3203-3213 of DRD2 in which
FT	there is a T at the polymorphic position
FT	3208"
XX	
XX	US5500343-A.
XX	

PD 19-MAR-1996.  
XX  
PF 07-FEB-1990; 90US-0477057.  
XX  
PR 24-JUN-1992; 92US-0909383.  
XX  
PR 07-FEB-1990; 90US-0477057.  
PR 23-JAN-1992; 92US-0826222.  
XX  
PA (REGC ) UNIV CALIFORNIA.  
PA (TEXA ) UNIV TEXAS SYSTEM.  
XX  
PI Blum K, Noble EP, Sheridan PJ;  
XX  
DR WPI; 1996-171043/17.  
XX  
PT Detecting genetic potential susceptibility to cocaine dependence or  
PT alcoholism - by detecting human dopamine D2 receptor gene A1 or B1  
PT allele in the subject's DNA  
XX  
PS Example 3; Column 45; 56pp; English.  
XX  
CC The dopamine D2 receptor DRD2(In6-Ex7) haplotype is comprised of  
CC two polymorphisms that are separated by 212 bp and span the  
CC junction of the intron 6 and exon 7 sequences. The first is a T or  
CC G at position 3208 and the second polymorphism is a T or C at  
CC position 3420, providing 4 possible haplotypes. Haplotype 1 is  
CC characterised by T at position 3208 and C at position 3420.  
CC The primers #3208 and #3420 specifically amplify a 241 bp fragment  
CC (3433-3193+1) beginning in intron 6 and ending in exon 7 of the  
CC dopamine D2 receptor haplotype 1 which is associated with  
CC alcoholism. The primers are used in a claimed method for detecting  
CC genetic potential susceptibility to alcoholism in human subjects.  
CC In particular, amplification is carried out using the PSA  
CC technique (i.e. PCR Amplification of Specific Alleles). In related  
CC methods, genetic potential susceptibility to cocaine dependence can  
CC be detected by amplifying human dopamine D2 receptor A1 and B1  
CC alleles (primers not specified).  
XX  
SQ Sequence 11 BP; 4 A; 0 C; 6 G; 1 T; 0 other;  
XX  
Query Match 100.0%; Score 10; DB 17; Length 11;  
Best Local Similarity 60.0%; Pred. No. 4.3e+03;  
Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CUUCCACCCU 10  
DB 11 CTTCCACCCT 2  
XX  
RESULT 12  
AA14846/c  
ID AA14846 standard; DNA; 12 BP.  
XX  
AC AA14846;  
XX  
DT 24-MAR-1999 (first entry)  
XX  
DE Triple helix forming nucleotides 384-395 of 23S rRNA gene.  
XX  
KW Triple-helix forming region; Triplex formation; DNA detection;  
KW identification; bacteria; oncogene; virus; ds.  
XX  
OS Leptospira interrogans.  
XX  
PN US5861244-A.  
XX  
PD 19-JAN-1999.  
XX  
PF 22-DEC-1993; 93US-0173489.  
XX  
PR 22-DEC-1993; 93US-0173489.  
PR 29-OCT-1992; 92US-0968436.  
XX

PA (PROF-) PROFILE DIAGNOSTIC SCI INC.  
XX  
PI Hepburn AG, Wang C;  
XX  
DR WPI; 1999-130384/11.  
XX  
PT Assay of genetic sequences based on triplex formation from double  
PT stranded analyte - and hybrid of anchor and reporter sequences, with  
PT reporter released if triplex formation occurs, used e.g. to identify  
PT bacteria  
XX  
PS Disclosure; Columns 21-22; 168pp; English.  
XX  
CC The present sequence represents a potential triple-helix forming region.  
CC It can be used to demonstrate the assay of the invention. The assay  
CC comprises adding a sample containing double-stranded DNA test sequences,  
CC e.g. containing the present sequence, to an aqueous medium containing at  
CC least one complex of anchor DNA, attached to a solid support, and  
CC reporter DNA, where either a part of the anchor DNA or reporter DNA is  
CC designed to form a triple-strand structure with part of the test  
CC sequence. Triplex formation results in displacement of the reporter DNA  
CC which is detected as an indication of the presence of the DNA test  
CC sequence. The method is used to detect DNA sequences, particularly for  
CC identification of bacteria (by detecting genes for ribosomal RNA) in  
CC clinical samples, but also detection of oncogenes and Hepatitis B virus.  
XX  
SQ Sequence 12 BP; 5 A; 0 C; 6 G; 1 T; 0 other;  
XX  
Query Match 100.0%; Score 10; DB 20; Length 12;  
Best Local Similarity 60.0%; Pred. No. 4.3e+03;  
Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CUUCCACCCU 10  
DB 12 CTTCCACCCT 3  
XX  
RESULT 13  
ABF08726/c  
ID ABF08726 standard; DNA; 13 BP.  
XX  
AC ABF08726;  
XX  
DT 21-FEB-2002 (first entry)  
XX  
DE Oligonucleotide SEQ ID NO 108723 for detecting SNP TSC0027206.  
XX  
KW SNP: single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX  
OS Homo sapiens.  
XX  
PN WO200177384-A2.  
XX  
PD 18-OCT-2001.  
XX  
PF 06-APR-2001; 2001WO-1B00713.  
XX  
PR 07-APR-2000; 2000DE-1019173.  
XX  
PA (EPIC-) EPIDEMIOLOGICS AG.  
XX  
PI Olek A, Plepenbrock C, Berlin K;  
XX  
DR WPI; 2001-657177/75.  
XX  
PT Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single nucleotide polymorphisms and cytosine  
PT methylation status  
XX  
PS Claim 1; SEQ ID 108723; 29pp + Sequence Listing; German.  
XX

CC This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation.  
CC ABC00010-ABC99989, ABF00010-ABF99989 and  
CC ABH00010-ABH82073 represent the oligomers described in the invention.  
CC NOTE: The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences.

Sequence 13 BP; 4 A; 0 C; 5 G; 4 T; 0 other;

Query Match 100.0%; Score 10; DB 23; Length 13;  
Best Local Similarity 60.0%; Pred. No. 4.3e+03;  
Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

OY 1 CUUUCACCCU 10  
13 CTTTCACCCCT 4

RESULT 14  
ABF08727

ID ABF08727 standard; DNA; 13 BP.

AC ABF08727;

DT 21-FEB-2002 (first entry)

DE Oligonucleotide SEQ ID NO 108724 for detecting SNP TSC0027206.

XX SNP: single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX  
OS Homo sapiens.

PN WO200177384-A2.

PD 18-OCT-2001.

PF 06-APR-2001; 2001WO-1B00713.

PR 07-APR-2000; 2000DE-1019173.

PS (EPIG-) EPIGENOMICS AG.

PI Olek A, Plepenbrock C, Berlin K;

DR WPI: 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single nucleotide polymorphisms and cytosine  
PT methylation status -

PS Claim 1; SEQ ID 108724; 29pp + Sequence Listing; German.

CC This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation.  
CC ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and  
CC ABH00010-ABH82073 represent the oligomers described in the invention.  
CC NOTE: The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences.

Sequence 13 BP; 4 A; 5 C; 0 G; 4 T; 0 other;

Query Match 100.0%; Score 10; DB 23; Length 13;  
Best Local Similarity 60.0%; Pred. No. 4.3e+03;  
Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

OY 1 CUUUCACCCU 10  
1 CTTTCACCCCT 10

RESULT 15  
ABH24716/C

ID ABH24716 standard; DNA; 13 BP.

AC ABH24716;

DT 22-FEB-2002 (first entry)

DE Oligonucleotide SEQ ID NO 224693 for detecting SNP TSC0054769.

XX SNP: single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX  
OS Homo sapiens.

PN WO200177384-A2.

PD 18-OCT-2001.

PF 06-APR-2001; 2001WO-1B00713.

PR 07-APR-2000; 2000DE-1019173.

PS (EPIG-) EPIGENOMICS AG.

PI Olek A, Plepenbrock C, Berlin K;

DR WPI: 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single nucleotide polymorphisms and cytosine  
PT methylation status -

PS Claim 1; SEQ ID 224693; 29pp + Sequence Listing; German.

CC This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation.  
CC ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and  
CC ABH00010-ABH82073 represent the oligomers described in the invention.  
CC NOTE: The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences.

Sequence 13 BP; 4 A; 0 C; 5 G; 4 T; 0 other;

Query Match 100.0%; Score 10; DB 23; Length 13;  
Best Local Similarity 60.0%; Pred. No. 4.3e+03;  
Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

OY 1 CUUUCACCCU 10  
10 CTTTCACCCCT 1

Search completed: March 19, 2003, 00:07:18  
Job time : 168 secs



GenCore version 5.1.4-p5.4578  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 19, 2003, 00:00:11 ; Search time 37 Seconds

(without alignments)  
82,886 Million cell updates/sec

Title: US-09-702-498A-33-MOD

Sequence: 1 CUUUCACCCU 10

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 441362 segs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08  
Maximum Match 1008  
Listing first 45 summaries

Database :

1: /cgn2\_6/pdata/1/lna/5A.COMB.seq:\*  
2: /cgn2\_6/pdata/1/lna/5B.COMB.seq:\*  
3: /cgn2\_6/pdata/1/lna/6A.COMB.seq:\*  
4: /cgn2\_6/pdata/1/lna/6B.COMB.seq:\*  
5: /cgn2\_6/pdata/1/lna/PCRTUS.COMB.seq:\*  
6: /cgn2\_6/pdata/1/lna/Backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	10	100.0	11	1	US-07-909-383-1
2	10	100.0	12	2	US-08-173-489C-233
3	10	100.0	19	3	US-08-777-266A-95
4	10	100.0	19	4	US-09-326-186B-95
5	10	100.0	22	3	US-08-777-266A-94
6	10	100.0	22	4	US-09-326-186B-94
7	10	100.0	23	1	US-07-952-442-7
8	10	100.0	23	1	US-08-269-766-7
9	10	100.0	23	1	US-08-319-545A-7
10	10	100.0	23	2	US-09-092-988-7
11	10	100.0	23	3	US-09-106-216-7
12	10	100.0	23	3	US-09-429-034-7
13	10	100.0	24	3	US-08-777-266A-93
14	10	100.0	24	4	US-09-326-186B-93
15	10	100.0	124	4	US-08-205-697A-39
16	10	100.0	124	4	US-08-702-5525-39
17	10	100.0	124	5	PCR-US95-02576-39
18	10	100.0	333	3	US-09-009-9115-15
19	10	100.0	337	2	US-08-702-652-40
20	10	100.0	337	6	5168053-1
21	10	100.0	397	4	US-08-636-597-2
22	10	100.0	397	4	US-09-232-063-2
23	10	100.0	438	4	US-09-228-986-56
24	10	100.0	440	4	US-09-397-787-321
25	10	100.0	584	4	US-09-328-111-83
26	10	100.0	616	4	US-09-328-111-574
27	10	100.0	650	4	US-09-328-111-189

28	10	100.0	650	4	US-09-404-879A-262	Sequence 262, App
29	10	100.0	676	4	US-09-221-017B-72	Sequence 72, Appl
30	10	100.0	709	1	US-08-469-667-12	Sequence 12, Appl
31	10	100.0	709	4	US-09-224-110-12	Sequence 12, Appl
32	10	100.0	709	5	PCR-US95-07289-12	Sequence 12, Appl
33	10	100.0	726	3	US-08-660-645A-11	Sequence 11, Appl
34	10	100.0	726	3	US-09-298-718-11	Sequence 11, Appl
35	10	100.0	726	4	US-09-546-969-11	Sequence 11, Appl
36	10	100.0	726	4	US-08-980-832-28	Sequence 28, Appl
37	10	100.0	747	4	US-09-134-001C-1462	Sequence 1462, Ap
38	10	100.0	771	1	US-08-253-155A-17	Sequence 17, Appl
39	10	100.0	778	2	US-08-781-560-2	Sequence 2, Appl
40	10	100.0	1013	6	5242798-8	Sequence 2, Appl
41	10	100.0	1036	3	US-09-267-031-9	Sequence 9, Appl
42	10	100.0	1037	4	US-09-535-008-57	Sequence 57, Appl
43	10	100.0	1103	4	US-08-936-165A-128	Sequence 128, App
44	10	100.0	1120	2	US-08-456-104-1	Sequence 1, Appl
45	10	100.0	1120	2	US-08-101-624-1	Sequence 1, Appl

#### ALIGNMENTS

RESULT 1  
US-07-909-383-1/C  
Sequence 1, Application US/07909383  
Patent No. 5500343  
GENERAL INFORMATION:  
APPLICANT: BLUM, KENNETH  
APPLICANT: NOBLE, E.P.  
TITLE OF INVENTION: SHERIDAN, P.J.  
TITLE OF INVENTION: ALLELIC ASSOCIATION OF THE HUMAN  
TITLE OF INVENTION: DOPAMINE (D2) RECEPTOR GENE IN  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: ARNOLD, WHITE & DUKREE  
STREET: P.O. BOX 4433  
CITY: HOUSTON  
STATE: TEXAS  
COUNTRY: USA  
ZIP: 77210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: FLOPPY DISK  
COMPUTER: IBM PC COMPATIBLE  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WORDPERECT 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/909,383  
FILING DATE: 19920624  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: HODGINS, DANIEL S.  
REGISTRATION NUMBER: 31,026  
REFERENCE/DOCKET NUMBER: US/TK:187  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 512-320-7200  
TELEFAX: 512-474-7577  
TELEX: NOT APPLICABLE  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 11 base pairs  
TYPE: NUCLEIC ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-07-909-383-1  
Query Match 100.0%; Score 10; Length 11;  
Best Local Similarity 60.0%; Pred. No. 6e+02;  
Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;  
1 CUUUCACCCU 10  
|:|||||:





LENGTH: 19  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthetic  
US-09-326-186B-95

Query Match  
Best Local Similarity 100.0%; Score 10; DB 4; Length 19;  
Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 CUUUCACCCU 10  
10 CTTTCACCCCT 16

RESULT 5  
US-08-777-266A-94  
Sequence 94, Application US/08777266A  
Patent No. 6077833

GENERAL INFORMATION:

APPLICANT: Clarence Frank Bennett

TITLE OF INVENTION: Oligonucleotide Compositions and

NUMBER OF SEQUENCES: 125  
METHODS for the Modulation of the Expression of B7 Proteins

CORRESPONDENCE ADDRESS:

ADDRESS: Law Offices of Jane Massey Licata

STREET: 210 Lake Drive East, Suite 201

CITY: Cherry Hill

STATE: NJ

COUNTRY: USA

ZIP: 08002

COMPUTER READABLE FORM:

MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE

COMPUTER: IBM PS/2

OPERATING SYSTEM: PC-DOS

SOFTWARE: WORDPERFECT 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/777,266A

FILING DATE: December 31, 1996

CLASSIFICATION: 536

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Jane Massey Licata

REGISTRATION NUMBER: 32,257

REFERENCE/DOCKET NUMBER: ISPH-0201

TELECOMMUNICATION INFORMATION:

TELEPHONE: (609) 779-2400

TELEFAX: (609) 779-8488

INFORMATION FOR SEQ ID NO: 94:

SEQUENCE CHARACTERISTICS:

LENGTH: 22

TYPE: Nucleic Acid

STRANDEDNESS: Single

TOPOLOGY: Linear

ANTI-SENSE: Yes

US-08-777-266A-94

Query Match  
Best Local Similarity 100.0%; Score 10; DB 3; Length 22;  
Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 CUUUCACCCU 10  
10 CTTTCACCCCT 19

RESULT 6  
US-09-326-186B-94  
Sequence 94, Application US/09326186B

Patent No. 6319906  
GENERAL INFORMATION:  
APPLICANT: Bennett, Clarence Frank  
APPLICANT: Vickers, Timothy A.  
TITLE OF INVENTION: Oligonucleotide Compositions and Methods for the  
MODULATION of the Expression of B7 Protein  
FILE REFERENCE: ISPH-0376  
CURRENT APPLICATION NUMBER: US/09/326,186B  
CURRENT FILING DATE: 1999-06-04  
PRIOR APPLICATION NUMBER: 08/777,266  
PRIOR FILING DATE: 1996-12-31  
NUMBER OF SEQ ID NOS: 226  
SOFTWARE: Patentln Ver. 2.0  
SEQ ID NO 94  
LENGTH: 22  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthetic  
US-09-326-186B-94

Query Match  
Best Local Similarity 100.0%; Score 10; DB 4; Length 22;  
Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 CUUUCACCCU 10  
10 CTTTCACCCCT 19

RESULT 7  
US-07-952-442-7  
Sequence 7, Application US/07952442  
Patent No. 5374525

GENERAL INFORMATION:

APPLICANT: Lalouel, Jean-Marc

APPLICANT: Jeunemaitre, Xavier

APPLICANT: Lifton, Richard P.

APPLICANT: Soubrrier, Florent

APPLICANT: Kotelevtsev, Youri

APPLICANT: Corval, Pierre

TITLE OF INVENTION: Angiogenesis Gene Variants and

NUMBER OF SEQUENCES: 22  
Predisposition to Essential Hypertension

CORRESPONDENCE ADDRESS:

ADDRESS: Venable, Baetjer, Howard & Civiletti

STREET: 1201 New York Avenue N.W., Suite 1000

CITY: Washington

STATE: DC

ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentln Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/952,442

FILING DATE: 19920930

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Ihnen, Jeffrey L.

REGISTRATION NUMBER: 28,957

REFERENCE/DOCKET NUMBER: 19780-104502

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-962-4810

TELEX: 202-962-8300

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

LENGTH: 23 base pairs

TYPE: NUCLEIC ACID

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
US-07-952-442-7

Query Match 100.0%; Score 10; DB 1; Length 23;  
Best Local Similarity 60.0%; Pred. No. 6.2e+02;  
Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

OY 1 CUUUCACCCU 10  
13 CTTTCACCCCT 22

RESULT 8  
US-08-269-766-7

Sequence 7, Application US/08269766  
Patent No. 5589584

GENERAL INFORMATION:

APPLICANT: Lalouel, Jean-Marc

APPLICANT: Jeunemaitre, Xavier

APPLICANT: Lifton, Richard P.

APPLICANT: Soubrier, Florent

APPLICANT: Kotelevtsev, Youri

APPLICANT: Corvol, Pierre

TITLE OF INVENTION: Angiotensinogen Gene Variants and

TITLE OF INVENTION: Predisposition to Essential Hypertension

NUMBER OF SEQUENCES: 22

CORRESPONDENCE ADDRESS:

ADDRESSEE: Venable, Baetjer, Howard & Civiletti

STREET: 1201 New York Avenue N.W., Suite 1000

CITY: Washington

STATE: DC

ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: IBM PC compatible

SOFTWARE: PC-DOS/MS-DOS

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/269,766

FILING DATE: 01-JUL-1994

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/952,442

FILING DATE: 30-SEP-1992

ATTORNEY/AGENT INFORMATION:

NAME: Ihnen, Jeffrey L.

REGISTRATION NUMBER: 28,957

REFERENCE/DOCKET NUMBER: 19780-104502

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-962-4810

TELEX: 202-962-8300

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

LENGTH: 23 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

HYPOTHETICAL: NO

ANTI-SENSE: NO

ORIGINAL SOURCE:

ORGANISM: Homo sapiens

DB 13 CTTTCACCCCT 22

RESULT 9  
US-08-319-545A-7

Sequence 7, Application US/08319545A  
Patent No. 5763168

GENERAL INFORMATION:

APPLICANT: Lalouel, Jean-Marc

APPLICANT: Jeunemaitre, Xavier

APPLICANT: Lifton, Richard P.

APPLICANT: Soubrier, Florent

APPLICANT: Kotelevtsev, Youri

APPLICANT: Corvol, Pierre

TITLE OF INVENTION: Method to Determine Predisposition

TITLE OF INVENTION: to Hypertension

NUMBER OF SEQUENCES: 22

CORRESPONDENCE ADDRESS:

ADDRESSEE: Venable, Baetjer, Howard & Civiletti

STREET: 1201 New York Avenue N.W., Suite 1000

CITY: Washington

STATE: DC

ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: IBM PC compatible

SOFTWARE: WordPerfect 5.1/5.2 Windows

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/319,545A

FILING DATE: 7-OCT-1994

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/952,442

FILING DATE: 30-SEP-1992

ATTORNEY/AGENT INFORMATION:

NAME: Ihnen, Jeffrey L.

REGISTRATION NUMBER: 28,957

REFERENCE/DOCKET NUMBER: 19780-104502-2

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-962-4810

TELEX: 202-962-8300

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

LENGTH: 23 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

HYPOTHETICAL: NO

ANTI-SENSE: NO

ORIGINAL SOURCE:

ORGANISM: Homo sapiens

US-08-319-545A-7

Query Match 100.0%; Score 10; DB 1; Length 23;  
Best Local Similarity 60.0%; Pred. No. 6.2e+02;  
Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

OY 1 CUUUCACCCU 10  
13 CTTTCACCCCT 22

RESULT 10  
US-09-092-988-7

Sequence 7, Application US/09092988  
Patent No. 5998145

GENERAL INFORMATION:

APPLICANT: Lalouel, Jean-Marc

APPLICANT: Jeunemaitre, Xavier

APPLICANT: Lifton, Richard P.

APPLICANT: Soubrier, Florent

APPLICANT: Kotelevtsev, Yuri  
APPLICANT: Corvol, Pierre  
TITLE OF INVENTION: Method to Determine Predisposition  
TITLE OF INVENTION: to Hypertension  
NUMBER OF SEQUENCES: 22  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Venable, Baetjer, Howard & Civiletti  
STREET: 1201 New York Avenue N.W., Suite 1000  
CITY: Washington  
STATE: DC  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WordPerfect 5.1/5.2 Windows  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/092,988  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/319,545  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Ihnen, Jeffrey L.  
REGISTRATION NUMBER: 28,957  
REFERENCE/DOCKET NUMBER: 19780-104502-2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-962-4810  
TELEFAX: 202-962-8300  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 23 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
US-09-092-988-7

Query Match  
Best Local Similarity 100.0%; Score 10; DB 2; Length 23;  
Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 CUUUCACCCU 10  
DB 13 CTTTCACCT 22

RESULT 11  
US-09-106-216-7  
Sequence 7, Application US/09106216  
Patent No. 6153386  
GENERAL INFORMATION:  
APPLICANT: Lalouel, Jean-Marc  
APPLICANT: Jeunemaitre, Xavier  
APPLICANT: Lifton, Richard P.  
APPLICANT: Soubrier, Florent  
APPLICANT: Kotelevtsev, Yuri  
APPLICANT: Corvol, Pierre  
TITLE OF INVENTION: Method to Determine Predisposition to  
TITLE OF INVENTION: Hypertension  
NUMBER OF SEQUENCES: 58  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Rothwell, Figg, Ernst & Kurz  
STREET: 555 Thirteenth Street N.W., Suite 701-E  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20004

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/106,216  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 09/  
FILING DATE: 08-JUN-1998  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/319,545  
FILING DATE: 07-OCT-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/952,545  
FILING DATE: 30-SEP-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Ihnen, Jeffrey L.  
REGISTRATION NUMBER: 28,957  
REFERENCE/DOCKET NUMBER: 2323-124  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-783-6040  
TELEFAX: 202-783-6031  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 23 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "primer"  
US-09-106-216-7

Query Match  
Best Local Similarity 100.0%; Score 10; DB 3; Length 23;  
Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 CUUUCACCCU 10  
DB 13 CTTTCACCT 22

RESULT 12  
US-09-429-034-7  
Sequence 7, Application US/09429034  
Patent No. 6165727  
GENERAL INFORMATION:  
APPLICANT: Lalouel, Jean-Marc  
APPLICANT: Jeunemaitre, Xavier  
APPLICANT: Lifton, Richard P.  
APPLICANT: Soubrier, Florent  
APPLICANT: Kotelevtsev, Yuri  
APPLICANT: Corvol, Pierre  
TITLE OF INVENTION: Method to Determine Predisposition  
TITLE OF INVENTION: to Hypertension  
NUMBER OF SEQUENCES: 22  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Venable, Baetjer, Howard & Civiletti  
STREET: 1201 New York Avenue N.W., Suite 1000  
CITY: Washington  
STATE: DC  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WordPerfect 5.1/5.2 Windows  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/429,034  
FILING DATE:  
CLASSIFICATION:

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/319,545  
FILING DATE: 7-OCT-1994  
APPLICATION NUMBER: US 07/952,442  
FILING DATE: 30-SEP-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Ihnen, Jeffrey L.  
REGISTRATION NUMBER: 28,957  
REFERENCE/DOCKET NUMBER: 19780-104502-2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-962-4810  
TELEX: 202-962-8300  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 23 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
US-09-429-034-7

Query Match 100.0%; Score 10; DB 4; Length 23;  
Best Local Similarity 60.0%; Pred. No. 6.2e+02;  
Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 CUUUCACCCU 10  
13 CTTTCACCCCT 22

RESULT 13  
US-08-777-266A-93  
Sequence 93, Application US/08777266A  
Patent No. 6077833  
GENERAL INFORMATION:  
APPLICANT: Clarence Frank Bennett  
APPLICANT: Timothy A. Vickers  
TITLE OF INVENTION: Oligonucleotide Compositions and  
TITLE OF INVENTION: Methods for the Modulation of the Expression of B7 Proteins  
NUMBER OF SEQUENCES: 125  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Law Offices of Jane Massey Licata  
STREET: 210 Lake Drive East, Suite 201  
CITY: Cherry Hill  
STATE: NJ  
COUNTRY: USA  
ZIP: 08002  
COMPUTER READABLE FORM:  
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE  
COMPUTER: IBM PS/2  
OPERATING SYSTEM: PC-DOS  
SOFTWARE: WORDPERFECT 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/777,266A  
FILING DATE: December 31, 1996  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Jane Massey Licata  
REGISTRATION NUMBER: 32,257  
REFERENCE/DOCKET NUMBER: ISPH-0201  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (609) 779-2400  
TELEFAX: (609) 779-8488  
INFORMATION FOR SEQ ID NO: 93:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 24

TYPE: Nucleic Acid  
STRANDEDNESS: Single  
TOPOLOGY: Linear  
ANTI-SENSE: Yes  
US-08-777-266A-93

Query Match 100.0%; Score 10; DB 3; Length 24;  
Best Local Similarity 60.0%; Pred. No. 6.2e+02;  
Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 CUUUCACCCU 10  
12 CTTTCACCCCT 21

RESULT 14  
US-09-326-186B-93  
Sequence 93, Application US/09326186B  
Patent No. 6319906  
GENERAL INFORMATION:  
APPLICANT: Bennett, Clarence Frank  
APPLICANT: Vickers, Timothy A.  
TITLE OF INVENTION: Oligonucleotide Compositions and Methods for the  
TITLE OF INVENTION: Modulation of the Expression of B7 Protein  
FILE REFERENCE: ISPH-0376  
CURRENT APPLICATION NUMBER: US/09/326,186B  
CURRENT FILING DATE: 1999-06-04  
PRIOR APPLICATION NUMBER: 08/777,266  
PRIOR FILING DATE: 1996-12-31  
NUMBER OF SEQ ID NOS: 226  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 93  
LENGTH: 24  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthetic  
US-09-326-186B-93

Query Match 100.0%; Score 10; DB 4; Length 24;  
Best Local Similarity 60.0%; Pred. No. 6.2e+02;  
Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 CUUUCACCCU 10  
12 CTTTCACCCCT 21

RESULT 15  
US-08-205-697A-39/C  
Sequence 39, Application US/08205697A  
Patent No. 6218510  
GENERAL INFORMATION:  
APPLICANT: Sharpe, Arlene H.  
APPLICANT: Borriello, Francescopaulo  
APPLICANT: Freeman, Gordon J.  
APPLICANT: Nadler, Lee M.  
TITLE OF INVENTION: No. 6218510el Forms of T Cell Costimulatory Molecules  
TITLE OF INVENTION: and Uses Therefor  
NUMBER OF SEQUENCES: 61  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LAHIVE & COCKFIELD  
STREET: 60 State Street, suite 510  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109-1875  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII Text  
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/205,697A  
FILING DATE: 02-Mar-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Mandragouras, Amy E.  
REGISTRATION NUMBER: 36,207  
REFERENCE/DOCKET NUMBER: BWI-120  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617)227-7400  
TELEFAX: (617)227-5941  
INFORMATION FOR SEQ ID NO: 39:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 124 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 107..124  
US-08-205-697A-39

Query Match 100.0%; Score 10; DB 4; Length 124;  
Best Local Similarity 60.0%; Pred. No. 6.9e+02;  
Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 CUUDCACCCT 10  
1::|||||:  
DB 13 CTTGCACCT 4

Search completed: March 19, 2003, 01:26:21  
Job time : 38 secs

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GenCore version 5.1.4.D5.4578  
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OM nucleic - nucleic search, using sw model

Run on: March 19, 2003, 00:40:46 ; Search time 51.5 Seconds

(without alignments)  
136.284 Million cell updates/sec

Title: US-09-702-498a-33-MOD

Perfect score: 10

Sequence: 1 CUUUCACCCU 10

IDENTITY\_NUC

Scoring table: Gapop 10.0, Gapext 1.0

Searched: 501302 seqs, 350932545 residues

Total number of hits satisfying chosen parameters: 1002604

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published\_Applications\_NA:\*  
1: /cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq:\*  
2: /cgn2\_6/ptodata/1/pubpna/PCCT\_NEM\_PUB.seq:\*  
3: /cgn2\_6/ptodata/1/pubpna/US06\_NEM\_PUB.seq:\*  
4: /cgn2\_6/ptodata/1/pubpna/US06\_PUBCOMB.seq:\*  
5: /cgn2\_6/ptodata/1/pubpna/US07\_NEM\_PUB.seq:\*  
6: /cgn2\_6/ptodata/1/pubpna/PCCTUS\_PUBCOMB.seq:\*  
7: /cgn2\_6/ptodata/1/pubpna/US08\_NEM\_PUB.seq:\*  
8: /cgn2\_6/ptodata/1/pubpna/US08\_PUBCOMB.seq:\*  
9: /cgn2\_6/ptodata/1/pubpna/US09\_NEM\_PUB.seq:\*  
10: /cgn2\_6/ptodata/1/pubpna/US09\_PUBCOMB.seq:\*  
11: /cgn2\_6/ptodata/1/pubpna/US10\_NEM\_PUB.seq:\*  
12: /cgn2\_6/ptodata/1/pubpna/US10\_PUBCOMB.seq:\*  
13: /cgn2\_6/ptodata/1/pubpna/US60\_NEM\_PUB.seq:\*  
14: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	10	100.0	10	9	US-09-966-277-63
2	10	100.0	10	9	US-09-966-930-63
3	10	100.0	10	10	US-09-823-699-1
4	10	100.0	21	10	US-09-972-331-21
5	10	100.0	30	9	US-09-988-115A-43
6	10	100.0	47	9	US-09-966-277-43
7	10	100.0	47	9	US-09-966-277-44
8	10	100.0	47	9	US-09-966-930-43
9	10	100.0	47	9	US-09-966-930-44
10	10	100.0	63	10	US-09-823-699-10
11	10	100.0	63	10	US-09-471-840-2
12	10	100.0	69	10	US-09-471-840-4
13	10	100.0	69	10	US-09-728-207-2
14	10	100.0	69	10	US-09-728-207-4
15	10	100.0	69	10	US-09-070-938-2
16	10	100.0	72	9	US-09-966-277-34
17	10	100.0	72	9	US-09-966-277-51
18	10	100.0	72	9	US-09-966-277-52
19	10	100.0	72	9	US-09-966-930-34

C	20	10	100.0	72	9	US-09-966-930-51	Sequence 51, Appl
C	21	10	100.0	72	9	US-09-966-930-52	Sequence 52, Appl
C	22	10	100.0	72	10	US-09-843-922-3	Sequence 3, Appl
C	23	10	100.0	74	9	US-09-966-277-31	Sequence 31, Appl
C	24	10	100.0	74	9	US-09-966-277-32	Sequence 32, Appl
C	25	10	100.0	74	9	US-09-966-930-31	Sequence 32, Appl
C	26	10	100.0	74	9	US-09-966-930-32	Sequence 32, Appl
C	27	10	100.0	80	9	US-09-966-277-18	Sequence 18, Appl
C	28	10	100.0	80	9	US-09-966-930-18	Sequence 18, Appl
C	29	10	100.0	112	10	US-09-783-590-8499	Sequence 8499, Ap
C	30	10	100.0	114	10	US-09-864-761-28324	Sequence 28324, A
C	31	10	100.0	116	10	US-09-864-761-24131	Sequence 24131, A
C	32	10	100.0	117	10	US-09-864-761-17517	Sequence 17517, A
C	33	10	100.0	124	9	US-09-962-969-39	Sequence 39, Appl
C	34	10	100.0	130	10	US-09-764-846-334	Sequence 334, Appl
C	35	10	100.0	132	10	US-09-869-373-1040	Sequence 1040, Ap
C	36	10	100.0	140	10	US-09-923-876-3943	Sequence 3943, Ap
C	37	10	100.0	143	10	US-09-783-590-7779	Sequence 7779, Ap
C	38	10	100.0	148	10	US-09-864-761-23518	Sequence 23518, A
C	39	10	100.0	165	9	US-10-046-935-156	Sequence 156, App
C	40	10	100.0	165	9	US-09-878-178-156	Sequence 156, App
C	41	10	100.0	165	10	US-09-864-761-30761	Sequence 30761, A
C	42	10	100.0	165	10	US-09-878-574-11498	Sequence 11498, A
C	43	10	100.0	174	10	US-09-783-590-6678	Sequence 6678, Ap
C	44	10	100.0	180	10	US-09-983-965-2379	Sequence 2379, Ap
C	45	10	100.0	180	10	US-09-983-965-2379	Sequence 2379, Ap

#### ALIGNMENTS

RESULT 1  
US-09-966-277-63  
Sequence 63, Application us/09966277  
Patient No. US20020169306A1  
GENERAL INFORMATION:  
APPLICANT: KITAZANO, Kato  
APPLICANT: SHU, Tsugumine  
APPLICANT: KOMA, Hidekazu  
APPLICANT: UEDA, Yasuji  
APPLICANT: ASAKAWA, Makoto  
APPLICANT: HASEGAWA, Mamoru  
APPLICANT: IIDA, Akihito  
APPLICANT: TOKITOU, Fumino  
APPLICANT: HIRATA, Takahiro  
APPLICANT: TOKUSUMI, Tsuyoshi  
APPLICANT: INOUE, Makoto  
TITLE OF INVENTION: ENVELOPE GENE-DEFICIENT PARAMYXOVIRUS  
TITLE OF INVENTION: VECTOR  
FILE REFERENCE: 50026/028001  
CURRENT APPLICATION NUMBER: US/09/966,277  
CURRENT FILING DATE: 2001-09-27  
PRIOR APPLICATION NUMBER: PCT/JP00/03195  
PRIOR FILING DATE: 2000-05-18  
PRIOR APPLICATION NUMBER: JP 2001/283451  
PRIOR FILING DATE: 2001-09-18  
PRIOR APPLICATION NUMBER: JP 11/200739  
PRIOR FILING DATE: 1999-05-18  
NUMBER OF SEQ ID NOS: 64  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 63  
LENGTH: 10  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Artificially Synthesized Sequence  
US-09-966-277-63

Query Match 100.0%; Score 10; DB 9; Length 10;  
Best Local Similarity 60.0%; Pred. No. 1.5e+03;  
Matches 6; Conservative 4; Mismatches 0; Indels 0;  
Gaps 0;  
Gy 1 CUUUCACCCU 10

Db 1 CTTTCACCT 10

## RESULT 2

US-09-966-930-63  
; Sequence 63, Application US/09966930  
; Publication No. US20030022376A1

## GENERAL INFORMATION:

APPLICANT: KITAZATO, Kaito  
APPLICANT: SHU, Tsugumine  
APPLICANT: KUMA, Hidekazu  
APPLICANT: UEDA, Yasuji  
APPLICANT: ASAKAWA, Makoto  
APPLICANT: HASEGAWA, Mamoru  
APPLICANT: IIDA, Akihiko  
APPLICANT: HIRATA, Takahiro  
APPLICANT: INOUE, Makoto  
TITLE OF INVENTION: PARAMYXOVIRUS-DERIVED RNP  
FILE REFERENCE: 50026/029001  
CURRENT FILING DATE: 2001-09-27  
PRIOR FILING DATE: 2000-05-18  
PRIOR APPLICATION NUMBER: JP 2001/283451  
PRIOR FILING DATE: 2001-09-18  
PRIOR APPLICATION NUMBER: JP 11/200740  
NUMBER OF SEQ ID NOS: 64  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 63  
LENGTH: 10  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Artificially Synthesized Sequence  
US-09-966-930-63

## Query Match

Best Local Similarity 100.0%; Score 10; DB 9; Length 10;  
Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 CUUUCACCCU 10  
Db 1 CTTTCACCT 10

## RESULT 3

US-09-823-699-1  
; Sequence 1, Application US/09823699  
; Patent No. US2002002143A1

## GENERAL INFORMATION:

APPLICANT: Kano, Munehide  
APPLICANT: Matano, Tetsuro  
APPLICANT: Kato, Atsushi  
APPLICANT: Nagai, Yoshiyuki  
APPLICANT: Hasegawa, Mamoru  
TITLE OF INVENTION: AIDS Virus Vaccines Using Sendai Virus  
FILE REFERENCE: 50026/022002  
CURRENT FILING DATE: US/09/823,699  
PRIOR FILING DATE: 2001-03-30  
PRIOR APPLICATION NUMBER: US 60/193,127  
NUMBER OF SEQ ID NOS: 18  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 1  
LENGTH: 10  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: artificially synthesized sequence  
US-09-823-699-1

Query Match 100.0%; Score 10; DB 10; Length 10;  
Best Local Similarity 60.0%; Pred. No. 1.5e+03;  
Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 CUUUCACCCU 10  
Db 1 CTTTCACCT 10

## RESULT 4

US-09-972-331-21/c  
; Sequence 21, Application US/09972331  
; Patent No. US20020091083A1

## GENERAL INFORMATION:

APPLICANT: HIGASHI, KIYOSHI  
APPLICANT: KONATSU, KENGO  
TITLE OF INVENTION: DNA-BINDING PROTEIN YB-1-CONTAINING  
FILE REFERENCE: 7372/72170  
CURRENT FILING DATE: US/09/972,331  
PRIOR FILING DATE: 2001-12-28  
PRIOR APPLICATION NUMBER: JP 2000/310624  
NUMBER OF SEQ ID NOS: 26  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 21  
LENGTH: 21  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: DESIGNED OLIGONUCLEOTIDE PRIMER TO SYNTHESIZE  
US-09-972-331-21

## Query Match

Best Local Similarity 100.0%; Score 10; DB 10; Length 21;  
Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 CUUUCACCCU 10  
Db 11 CTTTCACCT 2

## RESULT 5

US-09-988-115A-43  
; Sequence 43, Application US/09988115A  
; Publication No. US20030037347A1

## GENERAL INFORMATION:

APPLICANT: Robl, James M.  
APPLICANT: Goldsby, Richard A.  
APPLICANT: Ferguson, Stacy E.  
APPLICANT: Kuroiwa, Yoshitama  
APPLICANT: Tomizuka, Kazuma  
APPLICANT: Ishida, Isao  
TITLE OF INVENTION: Expression of Xenogenous (Human)  
FILE REFERENCE: 50195/008003  
CURRENT FILING DATE: Immunoglobulins in Cloned, Transgenic Ungulates  
CURRENT APPLICATION NUMBER: US/09/988,115A  
PRIOR FILING DATE: 2002-08-09  
PRIOR APPLICATION NUMBER: US 60/311,625  
PRIOR FILING DATE: 2001-08-09  
PRIOR APPLICATION NUMBER: US 60/256,458  
PRIOR FILING DATE: 2000-12-20  
PRIOR APPLICATION NUMBER: US 09/714,185  
PRIOR FILING DATE: 2000-11-17  
PRIOR APPLICATION NUMBER: US 60/166,410  
NUMBER OF SEQ ID NOS: 68  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 43  
LENGTH: 30  
TYPE: DNA



ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthetic Primer  
US-09-968-115A-43

Query Match 100.0%; Score 10; DB 9; Length 30;  
Best Local Similarity 60.0%; Pred. No. 1.1e+03;  
Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

OY 1 CUUUCACCCU 10  
13 CTTTCACCCCT 20

RESULT 6  
US-09-966-277-43/C  
Sequence 43, Application US/09966277  
Patent No. US20020169306A1  
GENERAL INFORMATION:

APPLICANT: KITAZARO, Kaio  
APPLICANT: SHU, Tsugumine  
APPLICANT: KUMA, Hidekazu  
APPLICANT: UEDA, Yasuji  
APPLICANT: ASAKAWA, Makoto  
APPLICANT: HASEGAWA, Mamoru  
APPLICANT: IIDA, Akihiro  
APPLICANT: TOKITOU, Fumino  
APPLICANT: HIRATA, Takahiro  
APPLICANT: TOKUSUMI, Tsuyoshi  
APPLICANT: INOUE, Makoto  
TITLE OF INVENTION: ENVELOPE GENE-DEFICIENT PARAMYXOVIRUS  
TITLE OF INVENTION: VECTOR  
FILE REFERENCE: 50026/028001  
CURRENT APPLICATION NUMBER: US/09/966,277  
PRIOR FILING DATE: 2001-09-27  
PRIOR APPLICATION NUMBER: PCT/JP00/03195  
PRIOR FILING DATE: 2000-05-18  
PRIOR APPLICATION NUMBER: JP 2001/283451  
PRIOR FILING DATE: 2001-09-18  
PRIOR APPLICATION NUMBER: JP 11/200739  
PRIOR FILING DATE: 1999-05-18  
NUMBER OF SEQ ID NOS: 64  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 43  
LENGTH: 47  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Artificially Synthesized Sequence  
US-09-966-277-43

Query Match 100.0%; Score 10; DB 9; Length 47;  
Best Local Similarity 60.0%; Pred. No. 1.1e+03;  
Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

OY 1 CUUUCACCCU 10  
13 CTTTCACCCCT 4

RESULT 7  
US-09-966-277-44  
Sequence 44, Application US/09966277  
Patent No. US20020169306A1  
GENERAL INFORMATION:

APPLICANT: KITAZARO, Kaio  
APPLICANT: SHU, Tsugumine  
APPLICANT: KUMA, Hidekazu  
APPLICANT: UEDA, Yasuji  
APPLICANT: ASAKAWA, Makoto  
APPLICANT: HASEGAWA, Mamoru  
APPLICANT: IIDA, Akihiro  
APPLICANT: TOKITOU, Fumino

APPLICANT: HIRATA, Takahiro  
APPLICANT: TOKUSUMI, Tsuyoshi  
APPLICANT: INOUE, Makoto  
TITLE OF INVENTION: ENVELOPE GENE-DEFICIENT PARAMYXOVIRUS  
TITLE OF INVENTION: VECTOR  
FILE REFERENCE: 50026/028001  
CURRENT APPLICATION NUMBER: US/09/966,277  
PRIOR FILING DATE: 2001-09-27  
PRIOR APPLICATION NUMBER: PCT/JP00/03195  
PRIOR FILING DATE: 2000-05-18  
PRIOR APPLICATION NUMBER: JP 2001/283451  
PRIOR FILING DATE: 2001-09-18  
PRIOR APPLICATION NUMBER: JP 11/200739  
PRIOR FILING DATE: 1999-05-18  
NUMBER OF SEQ ID NOS: 64  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 44  
LENGTH: 47  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Artificially Synthesized Sequence  
US-09-966-277-44

Query Match 100.0%; Score 10; DB 9; Length 47;  
Best Local Similarity 60.0%; Pred. No. 1.1e+03;  
Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

OY 1 CUUUCACCCU 10  
35 CTTTCACCCCT 44

RESULT 8  
US-09-966-930-43/C  
Sequence 43, Application US/09966930  
Publication No. US20030022376A1  
GENERAL INFORMATION:

APPLICANT: KITAZARO, Kaio  
APPLICANT: SHU, Tsugumine  
APPLICANT: KUMA, Hidekazu  
APPLICANT: UEDA, Yasuji  
APPLICANT: ASAKAWA, Makoto  
APPLICANT: HASEGAWA, Mamoru  
APPLICANT: IIDA, Akihiro  
APPLICANT: HIRATA, Takahiro  
APPLICANT: INOUE, Makoto  
TITLE OF INVENTION: PARAMYXOVIRUS-DERIVED RNP  
FILE REFERENCE: 50026/029001  
CURRENT APPLICATION NUMBER: US/09/966,930  
CURRENT FILING DATE: 2001-09-27  
PRIOR APPLICATION NUMBER: PCT/JP00/03194  
PRIOR FILING DATE: 2000-05-18  
PRIOR APPLICATION NUMBER: JP 2001/283451  
PRIOR FILING DATE: 2001-09-18  
PRIOR APPLICATION NUMBER: JP 11/200740  
PRIOR FILING DATE: 1999-05-18  
NUMBER OF SEQ ID NOS: 64  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 43  
LENGTH: 47  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Artificially Synthesized Sequence  
US-09-966-930-43

Query Match 100.0%; Score 10; DB 9; Length 47;  
Best Local Similarity 60.0%; Pred. No. 1.1e+03;  
Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

OY 1 CUUUCACCCU 10  
13 CTTTCACCCCT 4

OTHER INFORMATION: artificially synthesized sequence

EARLIER APPLICATION NUMBER: JP HEI 7-308315

EARLIER FILING DATE: 1996-10-22  
EARLIER APPLICATION NUMBER: 09/070,938  
NUMBER OF SEQ ID NOS: 6  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 4  
LENGTH: 69  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Chemical synthesis  
US-09-471-840-4

Query Match  
Best Local Similarity 100.0%; Score 10; DB 10; Length 69;  
Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

OY 1 CUUUCACCCU 10  
DB 16 CTTTCACCCCT 25

RESULT 13  
US-09-728-207-2  
Sequence 2, Application US/09728207  
Patent No. US20020098576A1  
GENERAL INFORMATION:  
APPLICANT: NAGAI, Yoshiyuki  
APPLICANT: KATO, Atsushi  
APPLICANT: MURAI, Fukashi  
APPLICANT: SAKATA, Tsuneaki  
APPLICANT: HASEGAWA, Mamoru  
APPLICANT: SHIODA, Tatsuo  
TITLE OF INVENTION: Recombinant Sendai Virus  
FILE REFERENCE: 50026/005001  
CURRENT APPLICATION NUMBER: US/09/728, 207  
CURRENT FILING DATE: 2000-12-01  
PRIOR APPLICATION NUMBER: US/09/071,591  
PRIOR FILING DATE: 1998-05-01  
PRIOR APPLICATION NUMBER: JP HEI 7-285417  
PRIOR FILING DATE: 1995-11-01  
PRIOR APPLICATION NUMBER: PCT/JP96/03069  
PRIOR FILING DATE: 1996-10-22  
NUMBER OF SEQ ID NOS: 6  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 2  
LENGTH: 69  
TYPE: DNA  
ORGANISM: Human Immunodeficiency Virus  
FEATURE:  
NAME/KEY: variation  
LOCATION: (35)...(35)  
OTHER INFORMATION: v at 35 is a, c, or g, not t or u.  
US-09-728-207-2

Query Match  
Best Local Similarity 100.0%; Score 10; DB 10; Length 69;  
Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

OY 1 CUUUCACCCU 10  
DB 17 CTTTCACCCCT 26

RESULT 14  
US-09-728-207-4  
Sequence 4, Application US/09728207  
Patent No. US20020098576A1  
GENERAL INFORMATION:  
APPLICANT: NAGAI, Yoshiyuki  
APPLICANT: KATO, Atsushi  
APPLICANT: MURAI, Fukashi  
APPLICANT: SAKATA, Tsuneaki

APPLICANT: HASEGAWA, Mamoru  
APPLICANT: SHIODA, Tatsuo  
TITLE OF INVENTION: Recombinant Sendai Virus  
FILE REFERENCE: 50026/005001  
CURRENT APPLICATION NUMBER: US/09/728, 207  
CURRENT FILING DATE: 2000-12-01  
PRIOR APPLICATION NUMBER: US/09/071,591  
PRIOR FILING DATE: 1998-05-01  
PRIOR APPLICATION NUMBER: JP HEI 7-285417  
PRIOR FILING DATE: 1995-11-01  
PRIOR APPLICATION NUMBER: PCT/JP96/03069  
PRIOR FILING DATE: 1996-10-22  
NUMBER OF SEQ ID NOS: 6  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 4  
LENGTH: 69  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Chemical synthesis  
US-09-728-207-4

Query Match  
Best Local Similarity 100.0%; Score 10; DB 10; Length 69;  
Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

OY 1 CUUUCACCCU 10  
DB 16 CTTTCACCCCT 25

RESULT 15  
US-09-070-938-2  
Sequence 2, Application US/09070938  
Patent No. US20020100066A1  
GENERAL INFORMATION:  
APPLICANT: Nagai, Yoshiyuki  
APPLICANT: Kato, Atsushi  
APPLICANT: Murai, Fukashi  
APPLICANT: Asakawa, Makoto  
APPLICANT: Sakata, Tsuneaki  
APPLICANT: Hasegawa, Mamoru  
APPLICANT: Shioda, Tatsuo  
TITLE OF INVENTION: Negative Strand RNA Viral  
TITLE OF INVENTION: Vector Having Autonomous Replication Capability  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Clark & Elbing LLP  
STREET: 176 Federal Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02110  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/070,938  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 7-308315  
FILING DATE: 31-OCT-1995  
APPLICATION NUMBER: JP96/03068  
FILING DATE: 22-OCT-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Clark, Paul T  
REGISTRATION NUMBER: 30,162  
REFERENCE/DOCKET NUMBER: 50026/004001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-428-0200

TELEFAX: 617-428-7045  
TELEX:  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 69 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other  
us-09-070-938-2

Query Match 100.0%; Score 10; DB 10; Length 69;  
Best Local Similarity 60.0%; Pred. NO. 1.9e+03;  
Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 CUUUCACCCU 10  
|:::|||||  
Db 17 CTTTCACCCU 26

Search completed: March 19, 2003, 02:47:57  
Job time : 51.5 secs

GenCore version 5.1.4-p5\_4578  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 18, 2003, 23:53:50 ; Search time 1320.5 Seconds

(without alignments)  
122.647 Million cell updates/sec

Title: US-09-702-498A-33-MOD

Sequence: 1 CUUCCACCCU 10

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 809774376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

Listing first 45 summaries

ESR: \*  
1: em\_estda: \*  
2: em\_esthm: \*  
3: em\_estln: \*  
4: em\_estlm: \*  
5: em\_estov: \*  
6: em\_estpl: \*  
7: em\_estro: \*  
8: em\_hic: \*  
9: gb\_est1: \*  
10: gb\_est2: \*  
11: gb\_hic: \*  
12: gb\_est3: \*  
13: gb\_est4: \*  
14: gb\_est5: \*  
15: em\_estfun: \*  
16: em\_estom: \*  
17: gb\_gss: \*  
18: em\_gss\_hum: \*  
19: em\_gss\_inv: \*  
20: em\_gss\_pla: \*  
21: em\_gss\_vit: \*  
22: em\_gss\_fun: \*  
23: em\_gss\_mam: \*  
24: em\_gss\_mus: \*  
25: em\_gss\_other: \*  
26: em\_gss\_pro: \*  
27: em\_gss\_rtd: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	100.0	28	17	TA285H020	AL485473 T. brucei
2	100.0	38	17	AZ332275	AZ332275 IM0060M11
3	100.0	43	17	AL754476	AL754476 Arabidops
4	100.0	67	17	AZ805524	AZ805524 2M0066P22
5	100.0	68	10	BE138421	BE138421 xrt74g04.x
6	100.0	72	13	BE1783611	BE1783611 kh33e05.Y.

7	100.0	72	17	AZ781553	AZ781553 2M0021103
8	100.0	73	17	B36161	B36161 HS-1038-A1-
9	100.0	80	17	FR0032825	FR0032825 Fugu rubr
10	100.0	84	13	B1550671	B1550671 603195845
11	100.0	88	17	BH405910	BH405910 RPTC-23-1
12	100.0	93	17	AZ659766	AZ659766 IM0537H21
13	100.0	93	17	AG101870	AG101870 Pan trogl
14	100.0	97	9	A1053527	A1053527 q172a01.x
15	100.0	97	9	A1053527	A1053527 q172a08.x
16	100.0	99	17	AZ829196	AZ829196 2M0106N07
17	100.0	99	17	AQ248921	AQ248921 F1833-T7.
18	100.0	101	13	BU091421	BU091421 BU091421
19	100.0	102	9	AA731433	AA731433 n294e01.s
20	100.0	103	13	BI004214	BI004214 MR4-HN005
21	100.0	103	17	AZ519083	AZ519083 RPTC-11-2
22	100.0	107	9	AT000717	AT000717 AT000717
23	100.0	108	9	AL840443	AL840443 AL840443
24	100.0	109	9	AA905844	AA905844 OJ87D05.8
25	100.0	109	10	BB594471	BB594471 BB594471
26	100.0	110	10	AM600553	AM600553 707053D02
27	100.0	110	12	BF987980	BF987980 CM0-GN016
28	100.0	110	13	BJ537314	BJ537314 BJ537314
29	100.0	110	17	BH809571	BH809571 KG07049-3
30	100.0	111	12	BG462159	BG462159 947077B11
31	100.0	112	9	A1499089	A1499089 t004e06.x
32	100.0	112	12	BG604174	BG604174 EST456372
33	100.0	112	13	BM191515	BM191515 da187d06.
34	100.0	112	14	W06033	W06033 TgESTzy80C0
35	100.0	113	12	BF910147	BF910147 CM2-UT008
36	100.0	114	13	BI037028	BI037028 CM1-WT020
37	100.0	115	17	BH088715	BH088715 RPTC-24-9
38	100.0	116	13	BI537374	BI537374 397189 MA
39	100.0	116	13	BJ209556	BJ209556 BJ209556
40	100.0	116	17	TA79G12P	TA79G12P T. brucei
41	100.0	117	12	BF992469	BF992469 I15-GN017
42	100.0	117	17	AQ385796	AQ385796 RPTC11-14
43	100.0	119	12	BG794168	BG794168 UTSW_SMC
44	100.0	120	12	BF604724	BF604724 270864 MA
45	100.0	121	12	BF174200	BF174200 MYE2738 M

## ALIGNMENTS

RESULT 1  
TA285H020  
LOCUS  
DEFINITION  
T. brucei sheared genomic DNA clone 285h02, reverse sequence.  
ACCSSION  
AL485473  
VERSION  
AL485473.1 GI:11853036  
KEYWORDS  
GSS.  
SOURCE  
Trypanosoma brucei.  
ORGANISM  
Trypanosoma.  
Eukaryota; Euzlenozoa; Kinetoplastida; Trypanosomatidae;  
1 (bases 1 to 28)

REFERENCE  
AUTHORS  
Hall, N., Bowman, S., Iennard, N.J., Doggett, J., Atkin, R.,  
Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,  
Melville, S.E., Rajandream, M.A. and Barrell, B.G.  
TITLE  
JOURNAL  
Direct Submision  
Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing  
project, Sanger Centre, The Wellcome Trust Genome Campus,  
Hinxton, Cambridge CB10 1SA. E-mail: barrellesanger.ac.uk and  
nhlesanger.ac.uk

COMMENT  
Constructed at the Institute for Genomic Research (TIGR),  
Rockville, MD. Genomic DNA isolated from a cloned population of  
Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared  
to give a tight size distribution (4 kb). The v + i method used for the library construction is  
described in detail in Smith, H. and Venter, J.C. (Making small  
insert libraries for whole genome shotgun sequencing projects. In  
Genome Sequencing: A Practical Approach, eds. M. Vaundin and B.

Barrell, Oxford University Press, 1999).  
 Email: nelsayed@tigr.org  
 Details of T. brucei sequencing at the Sanger Centre are available  
 at [http://www.sanger.ac.uk/Projects/T\\_brucei/](http://www.sanger.ac.uk/Projects/T_brucei/).

FEATURES  
 source  
 Location/Qualifiers  
 1. 28  
 /organism="Trypanosoma brucei"  
 /strain="PRE0927"  
 /db\_xref="taxon:5691"  
 /clone="285h02"

BASE COUNT  
 5 a 10 c 2 g 11 t  
 ORIGIN

Query Match 100.0%; Score 10; DB 17; Length 28;  
 Best Local Similarity 60.0%; Pred. No. 7.8e+04;  
 Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 CUUUCACCCU 10  
 Db 9 CTTTCACCCCT 18

RESULT 2  
 AZ332275/c 38 bp DNA linear GSS 29-SEP-2000  
 LOCUS  
 DEFINITION  
 1M0060M1R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
 clone UUGC1M0060M11 R. DNA sequence.  
 AZ332275  
 ACCESSION  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM

GSS.  
 house mouse.  
 Mus musculus

REFERENCE  
 AUTHORS  
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,  
 M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.  
 and Wright,D., Weis,R.  
 Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts

JOURNAL  
 COMMENT  
 Unpublished (2000)  
 Contact: Robert B. Weiss  
 University of Utah Genome Center  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0060 row: M column: 11  
 Seq primer: CACACAGGAACACGCTATGACC  
 Class: plasmid ends  
 High quality sequence stop: 38.

FEATURES  
 source  
 Location/Qualifiers  
 1. 38  
 /organism="Mus musculus"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUGC1M0060M11"  
 /clone\_11b="Mouse 10kb plasmid UUGC1M library"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /note="Vector: PWD42ny; Purified genomic DNA from M.  
 musculus C57BL/6J (male) was obtained from the Jackson  
 Laboratory Mouse DNA Resource  
 (<http://www.jax.org/resources/documents/dnares/>). The DNA  
 was hydrodynamically sheared by repeated passage through a  
 0.005 inch orifice at constant velocity. The sheared DNA  
 was blunt end-repaired with T4 DNA polymerase and T4  
 polynucleotide kinase. Adaptor oligonucleotides were  
 ligated to the blunt ends in high molar excess. The

BASE COUNT  
 10 a 8 c 15 g 5 t  
 ORIGIN

Query Match 100.0%; Score 10; DB 17; Length 38;  
 Best Local Similarity 60.0%; Pred. No. 8.3e+04;  
 Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 CUUUCACCCU 10  
 Db 19 CTTTCACCCCT 10

RESULT 3  
 AL754476 43 bp DNA linear GSS 17-JUN-2002  
 LOCUS  
 DEFINITION  
 Arabidopsis thaliana T-DNA flanking sequence GK-054E08-012357,  
 genomic survey sequence.  
 AL754476  
 ACCESSION  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM

GSS.  
 thale cress.  
 Arabidopsis thaliana

REFERENCE  
 AUTHORS  
 Strizhov,N., Li,Y., Rosso,M., Viehoever,P., Dekker,K., Saedler,H.  
 and Weisshaar,B.  
 A pipeline for automated high-throughput generation of ESTs  
 (flanking sequence tags) from Arabidopsis thaliana T-DNA  
 transformed lines  
 Unpublished

JOURNAL  
 COMMENT  
 Unpublished  
 Contact: Robert B. Weiss  
 University of Utah Genome Center  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0060 row: M column: 11  
 Seq primer: CACACAGGAACACGCTATGACC  
 Class: plasmid ends  
 High quality sequence stop: 38.

FEATURES  
 source  
 Location/Qualifiers  
 1. 43  
 /organism="Arabidopsis thaliana"  
 /strain="Columbia 0"  
 /db\_xref="taxon:3702"  
 /clone="GK-054E08-012357"  
 /clone\_11b="Arabidopsis thaliana T-DNA insertion lines"  
 /note="PCR was performed on DNA from Arabidopsis thaliana  
 plants (T1) which were transformed with the T-DNA from  
 vector pAc161. The lines contain one or more T-DNA  
 insertions. The DNA fragment(s) resulting from the PCR  
 were directly sequenced to determine the genomic sequence  
 flanking the insertion. Sequences displaying significant  
 similarity to the A. thaliana nuclear genome sequence were

adapted DNA was purified and size-selected for a 9.5 to  
 10.5 kb range using preparative agarose gel  
 electrophoresis. Vector DNA was prepared from a derivative  
 of PWD42 (g114732114|gb|AF129072.1), a copy-number  
 inducible derivative of plasmid R1. The vector was ligated  
 with adaptors complementary to the insert adaptors and  
 purified. The sheared, adapted mouse DNA was annealed to  
 adapted vector DNA, and transformed into  
 chemically-competent E. coli XL10-Gold (Stratagene) cells  
 and selected for ampicillin resistance.

Rosso,M., Strizhov,N., Li,Y., Reiss,B., Dekker,K. and Weisshaar,B.  
 A new Arabidopsis thaliana T-DNA mutagenised population (GABI-Kat)  
 for flanking sequence tag based reverse genetics  
 Unpublished  
 3 (bases 1 to 43)  
 Submitted (17-JUN-2002) Weisshaar,B., Max-Planck-Institut fuer  
 Zuechtungsforchung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany  
 This sequence is recovered from the left border of the T-DNA. It  
 indicates an insertion close to or within gene At3g07160. The  
 sequences are generated at the MPI for Plant Breeding Research in  
 the context of the GABI-Kat project. GABI-Kat is part of the German  
 plant genomics program designated 'GABI'. Information on line  
 availability can be found at:  
<http://www.mpiz-koeln.mpg.de/GABI-Kat/>.

processed for submission. T-DNA derived sequences were removed.

BASE COUNT 8 a 10 c 8 g 17 t

ORIGIN

Query Match 100.0%; Score 10; DB 17; Length 43;  
Best Local Similarity 60.0%; Pred. No. 8.5e+04;  
Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

OY 1 CUUUCACCCU 10  
1:::|||||:  
Db 33 CTTTCACCT 42

RESULT 4  
LOCUS A2805524 67 bp DNA linear GSS 20-FEB-2001  
DEFINITION 2M0066P22R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
ACCESSION A2805524  
VERSION A2805524.1 GI:12966335  
KEYWORDS GSS.  
SOURCE house mouse.  
ORGANISM Mus musculus

REFERENCE  
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 67)  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamill,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A. and Wright,D., Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunne@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0066 row: P column: 22  
Seq primer: CACACGAGAACGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 67.

#### FEATURES

SOURCE

1. 67  
Location/Qualifiers  
/organism="Mus musculus"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC2M0066P22"  
/clone\_11b="Mouse 10kb plasmid UUGC1M library"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (914732114[gb|AF129072.1]), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into

chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 23 a 13 c 17 g 14 t

ORIGIN

Query Match 100.0%; Score 10; DB 17; Length 67;  
Best Local Similarity 60.0%; Pred. No. 9.4e+04;  
Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

OY 1 CUUUCACCCU 10  
1:::|||||:  
Db 34 CTTTCACCT 25

RESULT 5  
LOCUS BE138421 68 bp mRNA linear EST 21-JUN-2000  
DEFINITION x174g04.x2 NCI-CGAP\_OV26 Homo sapiens cDNA clone IMAGE:2765910 3', mRNA sequence.  
ACCESSION BE138421  
VERSION BE138421.1 GI:8600921  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens

REFERENCE  
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 68)  
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index  
Unpublished (1997)  
Contact: Robert Strausberg, Ph.D.  
Email: cgapsb@mail.nih.gov  
Tissue Procurement: Monica Brown, M.D., Elise Kohn, M.D., Michael R. Emmert-Buck, M.D., Ph.D.  
cDNA Library Preparation: David B. Kitzman, Ph.D.  
cDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNt, send email to: info@image.lln.gov

TITLE Possible reversed clone: polyT not found  
JOURNAL Unpublished (1997)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapsb@mail.nih.gov  
Tissue Procurement: Monica Brown, M.D., Elise Kohn, M.D., Michael R. Emmert-Buck, M.D., Ph.D.  
cDNA Library Preparation: David B. Kitzman, Ph.D.  
cDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNt, send email to: info@image.lln.gov

#### FEATURES

SOURCE

1. 68  
Location/Qualifiers  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:2765910"  
/clone\_11b="NCI-CGAP\_OV26"  
/sex="Female"  
/tissue\_type="Papillary serous carcinoma"  
/dev\_stage="adult"  
/lab\_host="DH10B"  
/note="Organ: ovary; Vector: pAMP1; mRNA made from papillary serous ovarian carcinoma, cDNA made by oligo-dT priming. Directionally cloned. Size-selected on agarose gel, average insert size 500 bp. Primary library, non-amplified."  
BASE COUNT 26 a 8 c 22 g 12 t

Query Match 100.0%; Score 10; DB 10; Length 68;  
Best Local Similarity 60.0%; Pred. No. 9.4e+04;  
Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

OY 1 CUUUCACCCU 10  
1:::|||||:  
Db 57 CTTTCACCT 48

RESULT 6  
LOCUS BT783611 72 bp mRNA linear EST 26-SEP-2001

DEFINITION kh35e05.y1 Ascaris suum male head PAMPI v2 Chiapelli McCarter  
 ACCESSION A2781553  
 VERSION B1783611  
 KEYWORDS GI:15786503  
 SOURCE EST.  
 ORGANISM Ascaris suum  
 pig roundworm.  
 Eukaryota; Metazoa; Nematoda; Chromadorea; Ascaridida; Ascarididae  
 ; Ascarididae; Ascaris.  
 1 (bases 1 to 72)  
 McCarter, J., Clifton, S., Chiapelli, B., Pape, D., Martin, J., Wylie, T.,  
 Dante, M., Marra, M., Hillier, L., Kucaba, T., Theising, B., Bowers, Y.,  
 Gibbons, M., Rittler, E., Bennett, J., Franklin, C., Tsagaris, W., R.,  
 Ronko, I., Kennedy, S., Maguire, L., Beck, C., Underwood, K., Stepien,  
 M., Allen, M., Person, B., Swaller, T., Harvey, N., Schurk, R., Kohn, S.,  
 Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and  
 Wilson, R.  
 The Washington Univ. Nematode EST Project, 1999  
 Unpublished (1999)  
 TITLE The Washington Univ. Nematode EST Project, 1999  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: McCarter, J.P.  
 The Washington Univ. Nematode EST Project, 1999  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: est@watson.wustl.edu  
 The library was constructed by Brandi Chiapelli and Dr. James  
 McCarter at Washington University, St. Louis. The cDNA was made by  
 using Dynabead oligo-dT priming (Dynal). PCR based library using a  
 modified protocol from the SMART PCR cDNA Synthesis Kit from  
 Clontech. Directionally cloned into the UDG sites of PAMPI.  
 Dissected nematode tissues were provided by Dr. Alan Scott  
 (ascott@hsp.edu) of the School of Public Hygiene and Public Health  
 at John Hopkins University in Baltimore, MD.  
 Seq primer: -40RP from Gibco  
 High quality sequence stop: 58.  
 Location/Qualifiers  
 1..72  
 /organism="Ascaris suum"  
 /db\_xref="taxon:6253"  
 /clone\_lib="Ascaris suum male head PAMPI v2 Chiapelli  
 McCarter"  
 /sex="Male"  
 /tissue\_type="Head"  
 /dev\_stage="Adult"  
 /lab\_host="DH10B"  
 /note="Vector: PAMPI (Gibco); Site\_1: NotI; Site\_2: SalI;  
 The library was constructed by Brandi Chiapelli and Dr.  
 James McCarter at Washington University, St. Louis. The  
 cDNA was made by using Dynabead oligo-dT priming (Dynal).  
 PCR based library using a modified protocol from the SMART  
 PCR cDNA Synthesis Kit from Clontech. Directionally cloned  
 into the UDG sites of PAMPI. Dissected nematode tissues  
 were provided by Dr. Alan Scott (ascott@hsp.edu) of the  
 School of Public Hygiene and Public Health at John Hopkins  
 University in Baltimore, MD."  
 BASE COUNT 10 a 22 c 15 g 25 t  
 ORIGIN  
 Query Match 100.0%; Score 10; DB 13; Length 72;  
 Best Local Similarity 60.0%; Pred. No. 9.5e+04;  
 Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 CUUUCACCCU 10  
 Db 26 CTTTCACCT 35  
 RESULT 7 72 bp DNA linear GSS 16-FEB-2001  
 LOCUS A2781553  
 DEFINITION 2M0021103F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
 clone UUGC2M0021103 F, DNA sequence.

ACCESSION A2781553  
 VERSION A2781553.1  
 KEYWORDS GI:12914361  
 GSS.  
 SOURCE house mouse.  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sclerognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 72)  
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamli, C.,  
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,  
 M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.,  
 and Wright, D., Weiss, R.  
 Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts  
 Unpublished (2000)  
 TITLE Mouse whole genome scaffolding with paired end reads from 10kb  
 JOURNAL Unpublished (2000)  
 COMMENT Contact: Robert B. Weiss  
 University of Utah Genome Center  
 University of Utah  
 Rm 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLG, UT  
 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert length: 10000 Std Error: 0.00  
 Plate: 0021 row: 1 column: 03  
 Seq primer: CGTGTAAACGACGCCAGT  
 Class: plasmid ends  
 High quality sequence stop: 72.  
 Location/Qualifiers  
 1..72  
 /organism="Mus musculus"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUGC2M0021103"  
 /clone\_lib="Mouse 10kb plasmid UUGC1M library"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /note="Vector: PMD42nv; Purified genomic DNA from M.  
 musculus C57BL/6J (male) was obtained from the Jackson  
 Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA  
 was hydrodynamically sheared by repeated passage through a  
 0.005 inch orifice at constant velocity. The sheared DNA  
 was blunt end-repaired with T4 DNA polymerase and T4  
 polynucleotide kinase. Adaptor oligonucleotides were  
 ligated to the blunt ends in high molar excess. The  
 adaptor DNA was purified and size-selected for a 9.5 to  
 10.5 kb range using preparative agarose gel  
 electrophoresis. Vector DNA was prepared from a derivative  
 of pMD42 (g14732114/gb1AF129072.1), a copy-number  
 inducible derivative of plasmid R1. The vector was ligated  
 with adaptors complementary to the insert adaptors and  
 purified. The sheared, adaptor mouse DNA was annealed to  
 adaptor vector DNA, and transformed into  
 chemically-competent E. coli XL10-Gold (Stratagene) cells  
 and selected for ampicillin resistance."  
 BASE COUNT 5 a 26 c 3 g 38 t  
 ORIGIN  
 Query Match 100.0%; Score 10; DB 17; Length 72;  
 Best Local Similarity 60.0%; Pred. No. 9.5e+04;  
 Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 CUUUCACCCU 10  
 Db 34 CTTTCACCT 43  
 RESULT 8 73 bp DNA linear GSS 17-OCT-1997  
 LOCUS B36161  
 DEFINITION HS-1038-A1-E11-MF.ab1 CIT Human Genomic Sperm Library C Homo  
 sapiens genomic clone Plate=Ct 820 Col=21 Row=1, DNA sequence.



ACCESSION B36161  
 VERSION B36161.1 GI:2535530  
 KEYWORDS GSS.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
 1 (bases 1 to 73)  
 Mahairas,G.G., Zackrone,K.D., Smith,T., Tipton,S., Schmidt,S., Traicoff,R., Abajian,C., Blanchard,A., West,A. and Hood,L.E.  
 Construction of a Characterized Clone Resource for Genomic Sequencing: Generation and Preliminary Analysis of 20,000 Sequence Tagged Connectors  
 Unpublished (1997)  
 Contact: Mahairas GG, Zackrone KD, Hood L  
 University of Washington  
 Seattle, WA 98195, USA  
 Tel: (206) 616-8744  
 Fax: (206) 685-7301  
 Email: kzackrone@u.washington.edu  
 Sequence Tagged Connector  
 Plate: CT 820 row: I column: 21  
 Class: BAC ends  
 High quality sequence stop: 73.  
 Location/Qualifiers  
 1..73  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone="Plate-CT 820 Col-21 Row-I"  
 /clone.lib="CIR Human Genomic Sperm Library C"  
 /sex="M"  
 /note="Organ: sperm; Vector: pBelobAC11; BAC Clones in E-Coli DH10B"  
 BASE COUNT 21 a 14 c 21 g 16 t 1 others  
 ORIGIN  
 Query Match 100.0%; Score 10; DB 17; Length 73;  
 Best Local Similarity 60.0%; Pred. No. 9.6e+04;  
 Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 CUUUCACCCU 10  
 1:::|||||  
 Db 28 CTTTCACCT 19  
 RESULT 9  
 FR0032825 80 bp DNA linear GSS 27-JUN-1998  
 LOCUS Fugu rubripes GSS sequence, clone 152F05aG3, genomic survey  
 DEFINITION  
 sequence.  
 ACCESSION AL029193  
 VERSION AL029193.1 GI:3271307  
 KEYWORDS GSS; genome survey sequence.  
 SOURCE Takifugu rubripes.  
 ORGANISM Takifugu rubripes  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes; Tetraodontidae; Takifugu.  
 1 (bases 1 to 80)  
 Elgar,G., Clark,M., Smith,S., Meek,S., Warner,S., Umranta,Y., Williams,G. and Brenner,S.  
 Direct Submission  
 Submitted (09-JUN-1998) MRC Human Genome Mapping Project Resource Centre, Hinxton, Cambridge, CB10 1SB, UK. Email: biohelp@hgm.mrc.ac.uk  
 Vector: pBluescript II KS  
 V\_type: phagemid  
 PRIMER: KS  
 DESCR: One pass dye-terminator sequencing of cosmid cloned genomic sequence.  
 Location/Qualifiers  
 FEATURES  
 source  
 1..84  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:5275475"  
 /clone.lib="NIH\_MGC\_95"  
 /tissue.type="hippocampus"  
 /lab.host="DH10B"  
 /note="Organ: brain; Vector: pBluescript (modified pBluescript KS+); Site: 1: BamHI, Site: 2: SalI-XhoI (gtcgag); Oligo-dr primed using primer 5'-TTTTTTTTTTTTTNN-3', size-selected for average insert size 2.5 kb and normalized to ROT 5. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIH/NHGRI, National Institutes of Health). Note: this is a NIH\_MGC Library."  
 BASE COUNT 19 a 19 c 30 g 16 t  
 ORIGIN  
 Query Match 100.0%; Score 10; DB 13; Length 84;  
 Best Local Similarity 60.0%; Pred. No. 9.8e+04;  
 Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 CUUUCACCCU 10  
 1:::|||||  
 Db 21 CTTTCACCT 30

source  
 1..80  
 /organism="Takifugu rubripes"  
 /db\_xref="taxon:31033"  
 /clone="152F05aG3"  
 /clone.lib="cosmid 152F05"  
 BASE COUNT 7 a 22 c 13 g 35 t 3 others  
 ORIGIN  
 Query Match 100.0%; Score 10; DB 17; Length 80;  
 Best Local Similarity 60.0%; Pred. No. 9.7e+04;  
 Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 CUUUCACCCU 10  
 1:::|||||  
 Db 39 CTTTCACCT 48  
 RESULT 10  
 B1550671 84 bp mRNA linear EST 05-SEP-2001  
 LOCUS 603195845F1 NIH\_MGC\_95 Homo sapiens cDNA clone IMAGE:5275475 5',  
 DEFINITION mRNA sequence.  
 ACCESSION B1550671  
 VERSION B1550671 GI:15437983  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
 1 (bases 1 to 84)  
 NIH-MGC http://mhc.nci.nih.gov/.  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1993)  
 Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs-remail.nih.gov  
 Tissue Procurement: Miklos Palokovits, M.D., Ph.D.  
 cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shihaki Toshitsuki and Piero Carninci (RIKEN)  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  
 http://image.llnl.gov  
 Plate: LLM11695 row: 1 column: 12  
 High quality sequence stop: 84.  
 Location/Qualifiers  
 1..84  
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 /db\_xref="taxon:9606"  
 /clone="IMAGE:5275475"  
 /clone.lib="NIH\_MGC\_95"  
 /tissue.type="hippocampus"  
 /lab.host="DH10B"  
 /note="Organ: brain; Vector: pBluescript (modified pBluescript KS+); Site: 1: BamHI, Site: 2: SalI-XhoI (gtcgag); Oligo-dr primed using primer 5'-TTTTTTTTTTTTTNN-3', size-selected for average insert size 2.5 kb and normalized to ROT 5. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIH/NHGRI, National Institutes of Health). Note: this is a NIH\_MGC Library."  
 BASE COUNT 19 a 19 c 30 g 16 t  
 ORIGIN  
 Query Match 100.0%; Score 10; DB 13; Length 84;  
 Best Local Similarity 60.0%; Pred. No. 9.8e+04;  
 Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 CUUUCACCCU 10  
 1:::|||||  
 Db 21 CTTTCACCT 30

```

RESULT 11
BH405910
LOCUS      88 bp      DNA      linear      GSS 19-APR-2002
DEFINITION RPI-23-105F8.SP6E RPI-23 Mus musculus genomic clone RPI-23-105F8
            , DNA sequence.
ACCESSION  BH405910
VERSION     BH405910.1 GI:17460796
KEYWORDS
SOURCE      house mouse.
ORGANISM    Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1 (bases 1 to 88)
AUTHORS     Young,J.M., Friedman,C., Williams,E.M., Ross,J.A., Tonnes-Priddy,L.
            and Trask,B.J.
TITLE       Different evolutionary processes shaped the mouse and human
            olfactory receptor gene families
JOURNAL     Hum. Mol. Genet. 11 (5), 535-546 (2002)
MEDLINE     21864068
COMMENT     Contact: Young JM
            Barbara Trask, Division of Human Biology
            Fred Hutchinson Cancer Research Center
            1100 Fairview Avenue N., C3-168, P.O. Box 19024, Seattle, WA
            98109-1024, USA.
            Tel: 206 667 1471
            Fax: 206 667 6524
            Email: jayoung@fhcrc.org
            Young,J.M., Swartzell,S., Friedman,C., Tonnes-Priddy,L., Lane,R.P.,
            Wallace,J.C., Mahairas,G.G., Hood,L., and Trask,B.J. End sequences
            of mouse BACs containing olfactory receptor genes. Unpublished
            Plate: 105 row: F column: 8
            Seq primer: SP6E
            Class: BAC ends.

FEATURES
    source
        1..88
            /organism="Mus musculus"
            /strain="C57BL/6J"
            /db_xref="taxon:10090"
            /clone="RPI-23-105F8"
            /clone_1lb="RPI-23"
            /sex="Female"
            /lab_host="DH10B"
            /note="Organ: Kidney/Brain; Vector: pBAC3.6; Site: 1:
            EcoRI; Site 2: EcoRI; Female C57BL/6J mouse kidney and/or
            brain genomic DNA was isolated and partially digested
            with a combination of EcoRI and EcoRI MethyIase. Size
            selected DNA was cloned into the pBAC3.6 vector at the
            EcoRI sites. The ligation products were transformed into
            DH10B electrocompetent cells (BRL Life Technologies)."
BASE COUNT  19 a      34 c      11 g      24 t
ORIGIN
Query Match      100.0%; Score 10; DB 17; Length 88;
Best Local Similarity 60.0%; Pred. No. 9.9e+04;
Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

OY      1 CUUUCACCCU 10
Db      77 CTTTCACCT 86

RESULT 12
A2659766
LOCUS      93 bp      DNA      linear      GSS 14-DEC-2000
DEFINITION clone UUGC1M0537H21 F, DNA sequence.
ACCESSION  A2659766
VERSION     A2659766.1 GI:11796912
KEYWORDS
SOURCE      house mouse.
ORGANISM    Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```

```

REFERENCE   1 (bases 1 to 93)
AUTHORS     Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
            ,M., Rose,M., Rose,R., Stokes,R., Tingy,A., von Niederhausern,A.
            and Wright,D.,Weiss,R.
TITLE       Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
JOURNAL     Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SIC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000 Std Error: 0.00
            Plate: 0537 row: H column: 21
            Seq primer: CGTTGTAAACGACGCCACT
            Class: plasmid ends
            High quality sequence stop: 93.

FEATURES
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            /organism="Mus musculus"
            /strain="C57BL/6J"
            /db_xref="taxon:10090"
            /clone="UUGC1M0537H21"
            /clone_1lb="Mouse 10kb plasmid UUGC1M library"
            /sex="Male"
            /lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
            /note="Vector: pMD29ny. Purified genomic DNA from M.
            Laboratory Mouse DNA Resource
            (http://www.jax.org/resources/documents/dnares/). The DNA
            was hydrodynamically sheared by repeated passage through a
            0.005 inch orifice at constant velocity. The sheared DNA
            was blunt end-repaired with T4 DNA polymerase and T4
            polynucleotide kinase. Adaptor oligonucleotides were
            ligated to the blunt ends in high molar excess. The
            adaptor DNA was purified and size-selected for a 9.5 to
            10.5 kb range using preparative agarose gel
            electrophoresis. Vector DNA was prepared from a derivative
            of pMD22 (g1147321149b/AP129772.1), a copy-number
            inducible derivative of plasmid RL. The vector was ligated
            with adaptors complementary to the insert adaptors and
            purified. The sheared, adaptor mouse DNA was annealed to
            adaptor vector DNA, and transformed into
            chemically-competent E. coli XL10-Gold (Stratagene) cells
            and selected for ampicillin resistance."
BASE COUNT  17 a      30 c      20 g      26 t
ORIGIN
Query Match      100.0%; Score 10; DB 17; Length 93;
Best Local Similarity 60.0%; Pred. No. 1e+05;
Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

OY      1 CUUUCACCCU 10
Db      9 CTTTCACCT 18

RESULT 13
AG101870
LOCUS      93 bp      DNA      linear      GSS 03-NOV-2001
DEFINITION Pan troglodytes DNA, clone: PTB-105A03.R, genomic survey sequence.
ACCESSION  AG101870
VERSION     AG101870.1 GI:16722387
KEYWORDS
SOURCE      Pan troglodytes male lymphoblast DNA, clone_1lb:PTB Chimpanzee Male
            BAC library clone:PTB-105A03.R.
            Pan troglodytes
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```

REFERENCE 1 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Pan.  
AUTHORS Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T. D., Yada, T.,  
Totoki, Y., Watanabe, H. and Sakaki, Y.  
TITLE BAC end sequences of Library PTB  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 93)  
AUTHORS Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T. D., Yada, T.,  
Totoki, Y., Watanabe, H. and Sakaki, Y.  
TITLE Direct Submission  
JOURNAL Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical  
and Chemical Research (RIKEN), Genomic Sciences Center (GSC),  
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0043, Japan  
(E-mail: chimpbes@sc.riken.go.jp, URL: http://npg.gsc.riken.go.jp/,  
Tel: 81-45-503-9111, Fax: 81-45-503-9170)  
Clones are derived from the chimpanzee BAC library PTB. This BAC end  
was generated during the R&D process and may have higher chance of  
clone tracking errors.  
PRIMERS  
Sequencing: M13Rev  
LIBRARY  
Vector : pKS145  
R. Site 1 : SacI  
R. Site 2 : SacI  
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Best Local Similarity 60.0%; Pred. No. 1e+05;  
Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CUUUCACCCU 10  
1:::|||||  
Db 45 CTTTCACCC 54

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LOCUS q172a01.x1 NCI\_CGAP\_OV26 Homo sapiens cDNA clone IMAGE:1861992 3',  
DEFINITION mRNA sequence.  
ACCESSION AI053521  
VERSION AI053521.1 GI:3321308  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
1 (bases 1 to 97)  
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
Unpublished (1997)  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov  
Tissue Procurement: Monica Brown, M.D., Elise Kohn, M.D., Michael  
R. Emmert-Buck, M.D., Ph.D.  
CDNA Library Preparation: David B. Krizman, Ph.D.  
CDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LINL at:  
www-bio.lnlnl.gov/bdrp/image/image.html  
Seq primer: -40m13 fwd. ET from Amerisham.  
Location/Qualifiers

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/sex="female"  
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/dev\_stage="adult"  
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/note="Organ: ovary; Vector: PAMP1; mRNA made from  
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gel, average insert size 500 bp. Primary library,  
non-amplified."  
BASE COUNT 14 a 25 c 11 g 47 t  
ORIGIN  
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Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;  
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Db 32 CTTTCACCC 41

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DEFINITION mRNA sequence.  
ACCESSION AI053527  
VERSION AI053527.1 GI:3321314  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
1 (bases 1 to 97)  
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
Unpublished (1997)  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov  
Tissue Procurement: Monica Brown, M.D., Elise Kohn, M.D., Michael  
R. Emmert-Buck, M.D., Ph.D.  
CDNA Library Preparation: David B. Krizman, Ph.D.  
CDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LINL at:  
www-bio.lnlnl.gov/bdrp/image/image.html  
Seq primer: -40m13 fwd. ET from Amerisham.  
Location/Qualifiers

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non-amplified."  
BASE COUNT 14 a 25 c 12 g 46 t  
ORIGIN  
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Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 CUUUCACCCU 10  
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Db 31 CTTTCACCCU 40

Search completed: March 19, 2003, 01:24:58  
Job time : 1321.5 secs

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GenCore version 5.1.4-p5.4578  
Copyright (c) 1993 - 2003 Compugen Ltd.

## OM nucleic - nucleic search, using sw model

Run on: March 18, 2003, 23:07:15 ; Search time 991 Seconds

(without alignments)  
293.671 Million cell updates/sec

Title: US-09-702-498a-33

Perfect score: 10

Sequence: 1 CTTTCACCTT 10

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2054640 segs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

## Database :

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GenEmbl:
1: gb_ba:*
2: gb_hgt:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vl:*
30: em_hgt_hum:*
31: em_hgt_inv:*
32: em_hgt_other:*
33: em_hgt_mus:*
34: em_hgt_pin:*
35: em_hgt_rod:*
36: em_hgt_mam:*
37: em_hgt_vrt:*
38: em_sy:*
39: em_hgt_hum:*
40: em_hgt_mus:*
41: em_hgt_other:*
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	10	100.0	10	6 AX134713	AX134713 Sequence
2	10	100.0	10	6 AX477327	AX477327 Sequence
3	10	100.0	11	6 I18631	I18631 Sequence 1
4	10	100.0	12	6 AR030044	AR030044 Sequence
5	10	100.0	19	6 AR099568	AR099568 Sequence
6	10	100.0	19	6 AR178849	AR178849 Sequence
7	10	100.0	21	6 AX108449	AX108449 Sequence
8	10	100.0	21	6 AX108450	AX108450 Sequence
9	10	100.0	21	6 AX417439	AX417439 Sequence
10	10	100.0	21	6 AX476918	AX476918 Sequence
11	10	100.0	21	6 BD013048	BD013048 Paramyxov
12	10	100.0	21	6 BD013049	BD013049 Paramyxov
13	10	100.0	21	23 BD010081	BD010081 Paramyxov
14	10	100.0	21	23 BD010082	BD010082 Paramyxov
15	10	100.0	22	6 AR099567	AR099567 Sequence
16	10	100.0	22	6 AR178848	AR178848 Sequence
17	10	100.0	23	6 AR011837	AR011837 Sequence
18	10	100.0	23	6 AR092297	AR092297 Sequence
19	10	100.0	23	6 AR119514	AR119514 Sequence
20	10	100.0	23	6 AR122431	AR122431 Sequence
21	10	100.0	23	6 I33071	I33071 Sequence 7
22	10	100.0	24	6 AR099566	AR099566 Sequence
23	10	100.0	24	6 AR178847	AR178847 Sequence
24	10	100.0	47	6 BD011796	BD011796 RNP deriv
25	10	100.0	47	6 BD011797	BD011797 RNP deriv
26	10	100.0	47	23 BD004193	BD004193 RNP deriv
27	10	100.0	47	23 BD004194	BD004194 RNP deriv
28	10	100.0	53	6 A78690	A78690 Sequence 7
29	10	100.0	58	1 AF195107	AF195107 Sulfolobu
30	10	100.0	58	6 E47180	E47180 Process for
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32	10	100.0	64	23 BD010076	BD010076 Paramyxov
33	10	100.0	72	6 BD011787	BD011787 RNP deriv
34	10	100.0	72	6 BD011804	BD011804 RNP deriv
35	10	100.0	72	6 BD011805	BD011805 RNP deriv
36	10	100.0	72	23 BD004184	BD004184 RNP deriv
37	10	100.0	72	23 BD004201	BD004201 RNP deriv
38	10	100.0	72	23 BD004202	BD004202 RNP deriv
39	10	100.0	74	6 BD011784	BD011784 RNP deriv
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42	10	100.0	74	23 BD004182	BD004182 RNP deriv
43	10	100.0	76	6 AX134717	AX134717 Sequence
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45	10	100.0	80	23 BD004168	BD004168 RNP deriv

## ALIGNMENTS

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DEFINITION Sequence 1 from Patent WO0132898.
ACCESSION AX134713
VERSION AX134713.1 GI:14271230
KEYWORDS
SOURCE
ORGANISM
SYNTHETIC CONSTRUCT.
ARTIFICIAL SEQUENCES.
REFERENCE
1 (bases 1 to 10)
Yonemitsu,Y., Hasegawa,M. and Alton,E.
Recombinant sendai virus vector for introducing exogenous genes to
airway epithelia
JOURNAL Patent: WO 0132898-A 1 10-MAY-2001;
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FEATURES Dnavec Research Inc. (JP)  
Location/Qualifiers  
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Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 CTTTCACCT 10

RESULT 2  
AX477327 10 bp DNA linear PAT 12-AUG-2002  
LOCUS Sequence 1 from Patent WO0238726.  
ACCESSION AX477327  
VERSION AX477327.1 GI:22216577  
KEYWORDS  
SOURCE synthetic construct.  
ORGANISM synthetic construct  
REFERENCE 1  
AUTHORS Griesenbach,U., Ferrari,S., Geddes,D.M., Alton,E.W., Hasegawa,M.  
TITLE Paramyxovirus vector for gene transfer to the cardiovascular system  
JOURNAL Patent: WO 0238726-A 1 16-MAY-2002;  
Dnavec Research Inc. (JP)  
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Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 CTTTCACCT 10

RESULT 3  
I18631 11 bp DNA linear PAT 07-OCT-1996  
LOCUS Sequence 1 from patent US 5500343.  
ACCESSION I18631  
VERSION I18631.1 GI:1598986  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 11)  
AUTHORS Blum,K., Noble,E.P. and Sheridan,P.J.  
TITLE Allelic association of the human dopamine(D2) receptor gene in  
compulsive disorders  
JOURNAL Patent: US 5500343-A 1 19-MAR-1996;  
FEATURES Location/Qualifiers  
source 1. .11  
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DB 11 CTTTCACCT 2

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AR030044/C 12 bp DNA linear PAT 29-SEP-1999  
LOCUS AR030044  
DEFINITION Sequence 233 from patent US 5861244.  
ACCESSION AR030044  
VERSION AR030044.1 GI:5943258  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 12)  
AUTHORS Wang,C.-G. and Hepburn,A.G.  
TITLE Genetic sequence assay using DNA triple strand formation  
JOURNAL Patent: US 5861244-A 233 19-JAN-1999;  
FEATURES Location/Qualifiers  
source 1. .12  
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BASE COUNT 5 a 0 c 6 g 1 t  
ORIGIN

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Best Local Similarity 100.0%; Pred. No. 2.1e+05;  
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DB 12 CTTTCACCT 3

RESULT 5  
AR099568 19 bp DNA linear PAT 14-FEB-2001  
LOCUS AR099568  
DEFINITION Sequence 95 from patent US 6077833.  
ACCESSION AR099568  
VERSION AR099568.1 GI:12809334  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 19)  
AUTHORS Bennett,C.Frank, and Vickers,T.A.  
TITLE Oligonucleotide compositions and methods for the modulation of the  
expression of B7 protein  
JOURNAL Patent: US 6077833-A 95 20-JUN-2000;  
FEATURES Location/Qualifiers  
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DB 7 CTTTCACCT 16

RESULT 6  
AR178849 19 bp DNA linear PAT 20-APR-2002  
LOCUS AR178849  
DEFINITION Sequence 95 from patent US 6319906.  
ACCESSION AR178849  
VERSION AR178849.1 GI:20219987

KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 19)  
AUTHORS Bennett, C. Frank, and Vickers, T. A.  
TITLE Oligonucleotide compositions and methods for the modulation of the expression of B7 protein  
JOURNAL Patent: US 6319906-A 95-20-NOV-2001;  
FEATURES Location/Qualifiers  
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ORIGIN

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DB 7 CTTTCACCT 16

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AX108449/c 21 bp DNA linear PAT 30-APR-2001  
LOCUS AX108449  
DEFINITION Sequence 12 from Patent WO0123548.  
ACCESSION AX108449  
VERSION AX108449.1 GI:13923775  
KEYWORDS  
SOURCE synthetic construct.  
ORGANISM artificial sequences.  
REFERENCE 1 (bases 1 to 21)  
AUTHORS Dorit, R. L. and Cole, K. B.  
TITLE Dna-cleaving ribase p rna  
JOURNAL Patent: WO 0123548-A 12 05-APR-2001;  
FEATURES Location/Qualifiers  
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QY 1 CTTTCACCT 10  
DB 21 CTTTCACCT 12

RESULT 8  
AX108450 21 bp DNA linear PAT 30-APR-2001  
LOCUS AX108450  
DEFINITION Sequence 13 from Patent WO0123548.  
ACCESSION AX108450  
VERSION AX108450.1 GI:13923776  
KEYWORDS  
SOURCE synthetic construct.  
ORGANISM artificial sequences.  
REFERENCE 1 (bases 1 to 21)  
AUTHORS Dorit, R. L. and Cole, K. B.  
TITLE Dna-cleaving ribase p rna  
JOURNAL Patent: WO 0123548-A 13 05-APR-2001;  
FEATURES Location/Qualifiers  
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/note="primer"

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Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 CTTTCACCT 10

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AX417439/c 21 bp DNA linear PAT 18-JUN-2003  
LOCUS AX417439  
DEFINITION Sequence 21 from Patent EP197495.  
ACCESSION AX417439  
VERSION AX417439.1 GI:21522724  
KEYWORDS  
SOURCE synthetic construct.  
ORGANISM artificial sequences.  
REFERENCE 1  
AUTHORS Higashi, K. and Komatsu, K.  
TITLE Dna-binding protein yb-1-containing collagen accumulation inhibitors  
JOURNAL Patent: EP 1197495-A 21 17-APR-2002;  
FEATURES Sumitomo Chemical Company, Limited (JP)  
source Location/Qualifiers  
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/note="Designed oligonucleotide primer to synthesize collagen alpha 1 probe"

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QY 1 CTTTCACCT 10  
DB 11 CTTTCACCT 2

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LOCUS AX476918  
DEFINITION Sequence 9 from Patent WO0220848.  
ACCESSION AX476918  
VERSION AX476918.1 GI:22216171  
KEYWORDS  
SOURCE synthetic construct.  
ORGANISM artificial sequences.  
REFERENCE 1  
AUTHORS Bodnar, J. S., Castellani, L. W., Chatterjee, A., de Jong, P., Lusis, A. J., Olmen, J., Ross, D., Tafuri, S., and Wu, C.  
TITLE Gene and sequence variation associated with cancer  
JOURNAL Patent: WO 0220848-A 9 14-MAR-2002;  
FEATURES THE REGENTS OF THE UNIVERSITY OF CALIFORNIA (US)  
source Location/Qualifiers  
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RESULT 11						
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LOCUS	BD013048	21 bp	DNA	linear	PAT 02-AUG-2002	
DEFINITION	Paramyxovirus having modified transcription initiation sequence.					
ACCESSION	BD013048					
VERSION	MO 0118223-A/11.					
KEYWORDS	synthetic construct.					
SOURCE	synthetic construct.					
ORGANISM	artificial sequences.					
AUTHORS	1 (bases 1 to 21)					
TITLE	Nagai,Y., Kato,A. and Hasegawa,M.					
JOURNAL	Paramyxovirus having modified transcription initiation sequence					
COMMENT	Patent: WO 0118223-A 11 15-MAR-2001; DNAVEC RESEARCH INC,YOSHIYUKI NAGAI,ATSUSHI KATO,MAMORU HASEGAWA OS Artificial Sequence PN WO 0118223-A/11 PD 15-MAR-2001 PF 06-SEP-2000 WO 2000JP006051 PR 06-SEP-1999 JP 99P 252231 PI YOSHIYUKI NAGAI,ATSUSHI KATO,MAMORU HASEGAWA PC C12N15/86,C12N15/45//A61K31/7105,A61K48/00 CC Description of Artificial Sequence: artificially synthesized primer CC CC CC sequence FH Key Location/Qualifiers. source 1..21 /organism="synthetic construct" /db_xref="taxon:32630"					
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RESULT 12						
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DEFINITION	Paramyxovirus having modified transcription initiation sequence.					
ACCESSION	BD013049					
VERSION	MO 0118223-A/12.					
KEYWORDS	synthetic construct.					
SOURCE	synthetic construct.					
ORGANISM	artificial sequences.					
REFERENCE	1 (bases 1 to 21)					
AUTHORS	Nagai,Y., Kato,A. and Hasegawa,M.					
TITLE	Paramyxovirus having modified transcription initiation sequence					
JOURNAL	Patent: WO 0118223-A 12 15-MAR-2001; DNAVEC RESEARCH INC,YOSHIYUKI NAGAI,ATSUSHI KATO,MAMORU HASEGAWA OS Artificial Sequence PN WO 0118223-A/12 PD 15-MAR-2001 PF 06-SEP-2000 WO 2000JP006051 PR 06-SEP-1999 JP 99P 252231 PI YOSHIYUKI NAGAI,ATSUSHI KATO,MAMORU HASEGAWA					

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CC	7 a	6 g
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CC	Query Match	100.0%; Score 10; DB 6; Length 21;
CC	Best Local Similarity	100.0%; Pred. No. 1.9e+05;
CC	Matches 10; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
CC	1 CTTTCACCCT 10	
CC		
CC	9 CTTTCACCCT 18	
CC	RESULT 13	
CC	BD010081/c	
CC	ID BD010081	standard; DNA; SYN; 21 BP.
CC	BD010081;	
CC	BD010081.1	
CC	08-FEB-2002 (Rel. 70, Created)	
CC	08-FEB-2002 (Rel. 70, Last updated, Version 1)	
CC	Paramyxovirus having modified transcription initiation sequence.	
CC	JP 03075813-T/11.	
CC	synthetic construct	
CC	artificial sequence.	
CC	[1]	
CC	1-21	
CC	Nagai Y., Kato A., Hasegawa M.;	
CC	"Paramyxovirus having modified transcription initiation sequence";	
CC	Patent number JP03075813-T/11, 06-MAR-2001.	
CC	DNAVEC RESEARCH INC, YOSHIYUKI NAGAI, ATSUSHI KATO, MAMORU HASEGAWA.	
CC	OS Artificial Sequence	
CC	PN JP 03075813-T/11	
CC	PD 06-MAR-2001	
CC	PF 06-SEP-2000 JP 2000006051	
CC	PR 06-SEP-1999 JP 99P 252231	
CC	PI YOSHIYUKI NAGAI, ATSUSHI KATO, MAMORU HASEGAWA	
CC	C12N15/86, C12N15/45//A61K31/7105, A61K48/00	
CC	CC FH	Key
CC	CC FT	Location/Qualifiers
CC	1. .21	
CC	/organism="Artificial Sequence"	
CC	Key	Location/Qualifiers
CC	1. .21	
CC	source	Location/Qualifiers
CC	1. .21	
CC	/db_xref="taxon:32630"	
CC	/organism="synthetic construct"	
CC	Sequence 21 BP; 4 A; 4 C; 6 G; 7 T; 0 other;	
CC	Query Match	100.0%; Score 10; DB 23; Length 21;
CC	Best Local Similarity	100.0%; Pred. No. 1.9e+05;
CC	Matches 10; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
CC	1 CTTTCACCCT 10	
CC		



DB	13 CTTTCACCCCT 4
RESULT 14	
ID	BD010082 standard; DNA; SYN; 21 BP.
XX	BD010082;
AC	BD010082;
XX	BD010082.1
SV	BD010082.1
XX	
DT	08-FEB-2002 (Rel. 70, Created)
DT	08-FEB-2002 (Rel. 70, Last updated, Version 1)
DE	Paramyxovirus having modified transcription initiation sequence.
XX	JP 03075813-T/12.
KM	
XX	
OS	synthetic construct
OC	artificial sequence.
XX	
RN	[1]
RP	1-21
RA	Nagai Y., Kato A., Hasegawa M. ;
RT	"Paramyxovirus having modified transcription initiation sequence";
RL	Patent number JP03075813-T/12, 06-MAR-2001.
RL	DNAVEC RESEARCH INC, YOSHIIYUKI NAGAI, ATSUSHI KATO, MAMORU HASEGAWA.
XX	
CC	OS Artificial Sequence
CC	PN JP 03075813-T/12
CC	PD 06-MAR-2001
CC	PF 06-SEP-2000 JP 2000006051
CC	PR 06-SEP-1999 JP 99P 252231
CC	PI YOSHIIYUKI NAGAI,ATSUSHI KATO,MAMORU HASEGAWA
CC	C12NIJ5/86,C12NIJ5/45//A61K31/77105,A61K48/00
CC	
CC	FH Key
CC	FT source
XX	Location/Qualifiers
XX	1..21
XX	/organism="Artificial Sequence"
Key	Location/Qualifiers
source	1..21
	/db_xref="taxon:32630"
	/organism="synthetic construct"
Sequence	21 BP; 7 A; 6 C; 4 G; 4 T; 0 other;
Query Match	100.0%; Score 10; DB 23; Length 21;
Best Local Similarity	100.0%; Pred. No. 1.9e+05;
Matches	10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY	1 CTTTCACCCCT 10
Db	9 CTTTCACCCCT 18
RESULT 15	
LOCUS	AR099567 22 bp DNA linear PAT 14-FEB-2001
DEFINITION	Sequence 94 from patent US 6077833.
ACCESSION	AR099567
VERSION	AR099567.1 GI:12809333
KEYWORDS	
SOURCE	Unknown.
ORGANISM	Unknown.
REFERENCE	Unclassified.
AUTHORS	1 (bases 1 to 22)
TITLE	Bennett,C.Frank, and Vickers,T.A.
JOURNAL	Oligonucleotide compositions and methods for the modulation of the
FEATURES	expression of B7 protein Patent: US 6077833-A 94 20-JUN-2000; Location/Qualifiers

```

source          1. .22
                /organism="unknown"
BASE COUNT      6 a          6 c          5 g          5 t
ORIGIN
Query Match          100.0%; Score 10; DB 6; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.8e+05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY      1 CTTTCACCCCT 10
         |||||||||
Db      10 CTTTCACCCCT 19

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Search completed: March 19, 2003, 00:40:37  
Job time : 995 secs

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PT immunity comprises nasal administration to e.g. macaque to suppress  
PT onset and progress of AIDS -  
PS Disclosure: Page 27; 92pp; Japanese.  
XX  
XX The specification describes a vaccine containing a Sendai virus vector  
CC which encodes the viral protein of immunodeficiency virus. The vaccine  
CC is for treating AIDS, with expression of antigen gene mediated by the  
CC vector in nasal mucosa and local lymph nodes detected and  
CC antigen-specific cell-mediated response induced at significant  
CC level after vaccination. The present sequence represents an  
CC oligonucleotide which is used in the course of the invention.  
XX  
SQ Sequence 10 BP; 1 A; 5 C; 0 G; 4 T; 0 other;  
Query Match 100.0%; Score 10; DB 22; Length 10;  
Best Local Similarity 100.0%; Pred. No. 4.2e+03;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CTTTCACCCCT 10  
DB 1 CTTTCACCCCT 10  
RESULT 2  
AAH73613  
ID AAH73613 standard; DNA: 10 BP.  
XX  
XX AAH73613;  
AC  
XX  
XX 27-SEP-2001 (first entry)  
DT  
XX  
XX DNA sequence, SEQ ID NO: 1.  
DE  
XX  
XX Gene therapy: vascular disorder; recombinant paramyxovirus vector; ds.  
KM  
XX  
XX Unidentified.  
OS  
XX  
XX MO200153491-A1.  
PN  
XX  
XX 26-JUL-2001.  
PD  
XX  
XX 11-JAN-2001; 2001MO-JP00087.  
PF  
XX  
XX 19-JAN-2000; 2000JP-0014136.  
PR  
XX  
XX (DNAV-) DNAMEC RES INC.  
PA  
XX  
XX Masaki I, Yonemitsu Y, Sueishi K, Hasegawa M, Kinoh H;  
PI  
XX  
XX MPI; 2001-457610/49.  
DR  
XX  
XX Paramyxovirus vector containing foreign gene for efficient gene  
PT transfer into vascular cells -  
PT  
XX  
XX Disclosure: Page 19; 84pp; Japanese.  
PS  
XX  
XX The invention relates to a method for inserting nucleic acid into blood  
CC vessel cells by contacting the cells with the nucleic acid contained in a  
CC recombinant paramyxovirus vector or cells transformed by it. The  
CC method can be used for gene therapy of vascular disorders. Genes that  
CC can be introduced into blood vessel cells by this method include cell  
CC cycle regulators (such as p53, p21, p16 and p27), inhibitory factors  
CC (such as H-Ras, enos and C-natriuretic peptide), ion channels (such as  
CC Kir 6.2 potassium channel), blood proteins (such as urokinase and  
CC tissue plasminogen activator), tissue factor pathway inhibitors (such  
CC as TFPI) and vascular growth factors (such as vascular endothelial  
CC growth factor (VEGF), fibroblast growth factor (FGF) and hepatocyte  
CC growth factor (HGF)). The present sequence is provided in the  
CC specification.  
XX  
SQ Sequence 10 BP; 1 A; 5 C; 0 G; 4 T; 0 other;

Query Match 100.0%; Score 10; DB 22; Length 10;  
Best Local Similarity 100.0%; Pred. No. 4.2e+03;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CTTTCACCCCT 10  
DB 1 CTTTCACCCCT 10  
RESULT 3  
AAH23653  
ID AAH23653 standard; DNA: 10 BP.  
XX  
XX AAH23653;  
AC  
XX  
XX 07-AUG-2001 (first entry)  
DT  
XX  
XX S sequence oligonucleotide used in a recombinant Sendai virus vector.  
DE  
XX  
XX Gene therapy: S sequence; airway epithelium; cystic fibrosis; ds.  
KM  
XX  
XX Parainfluenza virus.  
OS  
XX  
XX MO200132898-A2.  
PN  
XX  
XX 10-MAY-2001.  
PD  
XX  
XX 02-NOV-2000; 2000MO-JP07737.  
PF  
XX  
XX 02-NOV-1999; 99US-0163055.  
PR  
XX  
XX 17-DEC-1999; 99JP-0359218.  
XX  
XX (DNAV-) DNAMEC RES INC.  
PA  
XX  
XX Yonemitsu Y, Hasegawa M, Alton EW;  
PI  
XX  
XX MPI; 2001-328799/34.  
DR  
XX  
XX New chorioallantoic fluid containing a recombinant Sendai virus vector  
PT carrying an exogenous gene, useful in gene therapy, particularly for  
PT treating cystic fibrosis in mammals, e.g. human, mouse, rabbit, sheep,  
PT bovine or monkey -  
PT  
XX  
XX Disclosure: Page 7; 42pp; English.  
PS  
XX  
XX The present invention relates to a composition for introducing exogenous  
CC genes to airway epithelia. The composition comprises a recombinant Sendai  
CC virus vector carrying an exogenous gene. The composition is useful in  
CC gene therapy. In particular, the composition is useful for treating  
CC cystic fibrosis in mammals, e.g. human, mouse, rabbit, sheep, bovine or  
CC monkey. The present sequence was used in the composition of the present  
CC invention as a transcription start sequence.  
XX  
SQ Sequence 10 BP; 1 A; 5 C; 0 G; 4 T; 0 other;  
Query Match 100.0%; Score 10; DB 22; Length 10;  
Best Local Similarity 100.0%; Pred. No. 4.2e+03;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CTTTCACCCCT 10  
DB 1 CTTTCACCCCT 10  
RESULT 4  
AAH86115  
ID AAH86115 standard; DNA: 10 BP.  
XX  
XX AAH86115;  
AC  
XX  
XX 21-JUN-2001 (first entry)  
DT  
XX  
XX Sendai virus S sequence oligonucleotide.  
DE

XX Extracellular superoxide dismutase; EC-SOD; immunosuppressive;  
 KW antiinflammatory; antiarthritis; antirheumatic; arthritis; colitis;  
 KW systemic autoimmune disease; systemic lupus erythematosus;  
 KW rheumatic myocarditis; progressive systemic sclerosis; dermatomyositis;  
 KW Sjogren's syndrome; polyarteritis; Sendai virus; ss.  
 XX  
 OS Parainfluenza virus.  
 XX  
 PN CA2316518-A1.  
 XX  
 PD 01-MAR-2001.  
 XX  
 PF 31-AUG-2000; 2000CA-2316518.  
 XX  
 PR 01-SEP-1999; 99JP-0248032.  
 PR 27-APR-2000; 2000CA-2304453.  
 XX  
 PA (DNAV-) DNA VEC RES INC.  
 XX  
 PI Yamauchi N, Fukumura M, Iyama S, Hasegawa M, Nitsui Y;  
 DR WPI; 2001-300717/32.  
 XX  
 PT New EC-SOD proteins and nucleic acids encoding the protein useful in  
 PT gene therapy for treating or preventing systemic autoimmune diseases,  
 PT e.g. rheumatoid arthritis, colitis and systemic lupus erythematosus -  
 XX  
 PS Disclosure; Page 24; 71pp; English.  
 XX  
 CC This invention relates to a superoxide dismutase (SOD) protein which  
 CC exists extracellularly and is termed EC-SOD, and the polynucleotide  
 CC encoding it. SOD is the enzyme that catalyses the reaction involved in  
 CC superoxide anion radical production. The invention includes a vector  
 CC containing the EC-SOD coding sequence, and a method for treating or  
 CC preventing systemic autoimmune diseases comprising administering the  
 CC vector. Methods using the EC-SOD protein and DNA sequences result in  
 CC immunosuppressive, anti-inflammatory, antiarthritis, and antirheumatic  
 CC activity. The EC-SOD protein and nucleic acid encoding the protein are  
 CC useful for treating systemic autoimmune diseases such as arthritis,  
 CC rheumatoid arthritis, colitis, systemic lupus erythematosus, rheumatic  
 CC myocarditis, progressive systemic sclerosis,  
 CC dermatomyositis/polyomyositis, mixed connective tissue disease, Sjogren's  
 CC syndrome, polyarteritis, Wegener granulomatosis and colitis. The present  
 CC sequence represents a Sendai virus (Parainfluenza virus) oligonucleotide  
 CC which can be used in the construction of a vector containing the EC-SOD  
 CC gene.  
 XX  
 SQ Sequence 10 BP; 1 A; 5 C; 0 G; 4 T; 0 other;  
 XX  
 Query Match 100.0%; Score 10; DB 22; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 4.2e+03;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 1 CTTTCACCCCT 10  
 |||||||||  
 DB 1 CTTTCACCCCT 10  
 RESULT 5  
 AAF77598  
 ID AAF77598 standard; DNA; 10 BP.  
 XX  
 AC AAF77598;  
 XX  
 DT 29-MAY-2001 (first entry)  
 XX  
 DE Modified transcription initiation site Paramyxovirus related oligo #18.  
 XX  
 KW Transcription initiation sequence; viral vector; vaccine; therapy; ds.  
 OS Unidentified.  
 XX

PN W0200118223-A1.  
 XX  
 PD 15-MAR-2001.  
 XX  
 PF 06-SEP-2000; 2000MO-JP06051.  
 XX  
 PR 06-SEP-1999; 99JP-02522231.  
 XX  
 PA (DNAV-) DNAVEC RES INC.  
 XX  
 PI Nagai Y, Kato A, Hasegawa M;  
 DR WPI; 2001-244576/25.  
 XX  
 PT Paramyxovirus vectors with modified transcription initiation sequences  
 PT for increased expression of foreign genes in production of drugs and  
 PT vaccines -  
 XX  
 PS Disclosure; Page 17; 65pp; Japanese.  
 XX  
 CC The present invention describes a paramyxovirus vector DNA in which the  
 CC transcription initiation sequence has been modified to modify the  
 CC expression of a gene located downstream of the transcription initiation  
 CC sequence. This is useful in the production of mutant paramyxovirus  
 CC vectors with elevated gene expression and a more rapid proliferation than  
 CC the wild-type vector, which can then be used for more efficient  
 CC production of drug substances and vaccines.  
 XX  
 SQ Sequence 10 BP; 1 A; 5 C; 0 G; 4 T; 0 other;  
 XX  
 Query Match 100.0%; Score 10; DB 22; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 4.2e+03;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 1 CTTTCACCCCT 10  
 |||||||||  
 DB 1 CTTTCACCCCT 10  
 RESULT 6  
 AAL47265  
 ID AAL47265 standard; DNA; 10 BP.  
 XX  
 AC AAL47265;  
 XX  
 DT 30-AUG-2002 (first entry)  
 XX  
 DE Sendai virus S sequence complement.  
 XX  
 KW Sendai virus vector; gene therapy; antiinflammatory; inflammation;  
 KW cardiovascular system; paramyxovirus; IL-10; pulmonary fibrosis;  
 KW sclerosing peritonitis; prostatomegaly; multiple sclerosis;  
 KW neuroprotective; immunosuppressive; antidiabetic; antirheumatic;  
 KW transplant rejection; diabetes; chronic articular rheumatism;  
 KW psoriasis; inflammatory enteropathy; systemic lupus erythematosus;  
 KW lritis; granulomatous disease; chronic nephritis; scleroderma;  
 KW hystereomyoma; keloid; cirrhosis; cystic fibrosis; pneumonia; ss.  
 XX  
 OS Sendai virus.  
 XX  
 PN W0200238726-A2.  
 XX  
 PD 16-MAY-2002.  
 XX  
 PF 08-NOV-2001; 2001MO-JP09786.  
 XX  
 PR 08-NOV-2000; 2000JP-0339942.  
 XX  
 PA (DNAV-) DNAVEC RES INC.  
 XX  
 PI Griesenbach U, Ferrari S, Geddes DM, Alton EW, Hasegawa M, Hou X;  
 DR WPI; 2002-490069/52.

XX Novel paramyxovirus vector for gene transfer to cardiovascular system,  
PT in which expression product of gene comprised in vector is transferred  
PT to a site different from the site of administration through the  
PT bloodstream  
PS Disclosure: Page 17; 67pp; English.

XX The present invention relates to a paramyxovirus vector for gene transfer  
CC to the cardiovascular system, where the expression product of a gene  
CC comprised in the vector is transferred to a site different from the site  
CC of administration through the bloodstream. The vector is useful for  
CC transferring sequences such as IL-10 to the cardiovascular system, for  
CC treating pneumonia in cystic fibrosis patients and for treating  
CC inflammatory diseases such as pulmonary fibrosis, sclerosing peritonitis,  
CC proctocolitis, multiple sclerosis, post transplant rejection, diabetes,  
CC chronic articular rheumatism, psoriasis, inflammatory enteropathy,  
CC systemic lupus erythematosus, iritis, granulomatous disease, chronic  
CC nephritis, scleroderma, hysteromyoma, keloid and cirrhosis. The present  
CC sequence is a DNA fragment used to produce the vector of the invention.

XX Sequence 10 BP; 1 A; 5 C; 0 G; 4 T; 0 other;

Query Match 100.0%; Score 10; DB 24; Length 10;  
Best Local Similarity 100.0%; Pred. No. 4.2e+03;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CTTTCACCT 10  
DB 1 CTTTCACCT 10

RESULT 7  
ABL38107  
ID AAL38107 standard; DNA; 10 BP.  
XX AAL38107;  
AC AAL38107;  
XX 15-AUG-2002 (first entry)  
DT 15-AUG-2002 (first entry)  
XX Angiogenesis gene containing paramyxovirus vector related oligo #1.  
DE Angiogenesis gene containing paramyxovirus vector related oligo #1.  
XX Vasotropic; paramyxovirus vector; angiogenesis gene; gene therapy; FGF2;  
KM Ischaemia; virus vector; edema; tissue targeting; ds.  
XX Undeidentified.  
OS WO200242481-A1.  
PN WO200242481-A1.  
XX 30-MAY-2002.  
PD 30-MAY-2002.  
XX 27-NOV-2001; 2001WO-JP10323.  
PF 27-NOV-2001; 2001WO-JP10323.  
XX 27-NOV-2000; 2000JP-0359374.  
PR 27-NOV-2000; 2000JP-0359374.  
XX (DNAV-) DNAVEC RES INC.  
PA (DNAV-) DNAVEC RES INC.  
XX Yonemitsu Y, Sueishi K, Fukumura M, Hou X, Hasegawa M;  
PI WPI: 2002-452662/48.  
XX WPI: 2002-452662/48.  
DR WPI: 2002-452662/48.  
XX Paramyxovirus vector containing angiogenesis gene FGF2 for gene therapy  
PT treatment targeting ischemic tissue  
PT treatment targeting ischemic tissue  
XX Disclosure: Page 23; 94pp; Japanese.  
PS The invention relates to a paramyxovirus vector containing an  
CC angiogenesis gene, which can be used for gene therapy of ischaemia in  
CC tissues including brain, heart, lung, skeletal muscle and kidney. The  
CC expression of the virus vector is free from edema and specific tissues  
CC can be targeted. This polynucleotide sequence represents an artificial  
CC oligonucleotide relating to the paramyxovirus vector containing an  
CC angiogenesis gene FGF2 of the invention.

XX Sequence 10 BP; 1 A; 5 C; 0 G; 4 T; 0 other;

Query Match 100.0%; Score 10; DB 24; Length 10;  
Best Local Similarity 100.0%; Pred. No. 4.2e+03;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CTTTCACCT 10  
DB 1 CTTTCACCT 10

RESULT 8  
ABK48812  
ID ABK48812 standard; DNA; 10 BP.  
XX ABK48812;  
AC ABK48812;  
XX 15-JUL-2002 (first entry)  
DT 15-JUL-2002 (first entry)  
XX DNA sequence #1 relating to paramyxovirus vector for gene transfer.  
DE DNA sequence #1 relating to paramyxovirus vector for gene transfer.  
XX Method for gene transfer; skeletal muscle; paramyxovirus vector;  
KM gene therapy; neuromuscular disorder; tumourigenesis; neuroprotective;  
KM myotropic; insulin-like growth factor; IGF; ds.  
XX Undeidentified.  
OS WO200231138-A1.  
PN WO200231138-A1.  
XX 18-APR-2002.  
PD 18-APR-2002.  
XX 26-SEP-2001; 2001WO-JP08372.  
PF 26-SEP-2001; 2001WO-JP08372.  
XX 06-OCT-2000; 2000JP-0308533.  
PR 06-OCT-2000; 2000JP-0308533.  
XX (DNAV-) DNAVEC RES INC.  
PA (DNAV-) DNAVEC RES INC.  
XX Hukumura M, Shiotani A, Maeda M, Hasegawa M;  
PI WPI: 2002-340180/37.  
XX WPI: 2002-340180/37.  
DR WPI: 2002-340180/37.  
XX Paramyxovirus vector for transferring foreign gene e.g. insulin-like  
PT growth factor into skeletal muscle in gene therapy of neuromuscular  
PT disorders  
PT disorders  
XX Disclosure: Page 14; 56pp; Japanese.  
PS The present invention relates to a method for transferring a foreign  
CC gene into skeletal muscle. The method comprises administering a  
CC paramyxovirus inserted with the foreign gene. The paramyxovirus vector  
CC is useful for transferring a foreign gene e.g. insulin-like growth  
CC factor (IGF) into skeletal muscle in the gene therapy of neuromuscular  
CC disorders. Such a vector can sustain transgene expression for up to a  
CC month after injection and is safe, non-infective and does not cause  
CC tumourigenesis. The present DNA sequence of unknown function is  
CC given in the specification of the present invention.

XX Sequence 10 BP; 1 A; 5 C; 0 G; 4 T; 0 other;

Query Match 100.0%; Score 10; DB 24; Length 10;  
Best Local Similarity 100.0%; Pred. No. 4.2e+03;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CTTTCACCT 10  
DB 1 CTTTCACCT 10

RESULT 9  
ABL39904  
ID ABL39904 standard; DNA; 10 BP.  
XX ABL39904 standard; DNA; 10 BP.

AC ABL39904;  
 XX  
 DT 14-MAY-2002 (first entry)  
 XX  
 DE Sendai virus S oligonucleotide SEQ ID NO:1.  
 XX  
 KW Sendai virus; virus vector; renal cell; paramyxovirus; gene transfer;  
 KW gene therapy; kidney; nephrotropic; antidiabetic; diabetes; renopathy;  
 KW chronic glomerulonephritis; glomerulosclerosis; Allport's syndrome;  
 KW tubulointerstitial nephritis; ss.  
 XX  
 OS Parainfluenza virus.  
 XX  
 PN WO200200264-A1.  
 XX  
 PD 03-JAN-2002.  
 XX  
 PF 27-JUN-2001; 2001WO-JP05513.  
 XX  
 PR 27-JUN-2000; 2000JP-0197870.  
 XX  
 PA (DNAV-) DNAVEC RES INC.  
 XX  
 PI Imai E, Isaka Y, Fukumura M, Hasegawa M;  
 XX  
 DR WPI; 2002-130841/17.  
 XX  
 PT Transferring a gene into renal cells, useful for gene therapy of a  
 PT kidney to treat e.g. chronic glomerulonephritis, comprises using a  
 PT virus vector particularly of paramyxovirus  
 XX  
 PS Example 1; Page 38; 75pp; Japanese.  
 XX  
 CC The present invention describes transferring a gene into renal cells  
 CC comprising contacting a paramyxovirus vector with the renal cells,  
 CC particularly by administration into blood vessels, especially the renal  
 CC artery or into the urethra. Also described are: (1) a paramyxovirus  
 CC vector for use in transferring a gene into renal cells; and  
 CC (2) compositions for transferring a gene into renal cells comprising  
 CC cells having the paramyxovirus vector or the vector. The method is used  
 CC for transferring a gene into renal cells. The virus is applicable in  
 CC gene therapy for the kidney to treat target diseases of e.g. chronic  
 CC glomerulonephritis, diabetes, renopathy, glomerulosclerosis,  
 CC tubulointerstitial nephritis and Allport's syndrome. The transfer of a  
 CC gene into renal cells is with high efficiency, and after brief exposure,  
 CC the transferred gene is continuously expressed in renal cells over a  
 CC long period of time. The present sequence represents a Sendai virus  
 CC (parainfluenza virus) oligonucleotide which is used in an example from  
 CC the present invention.  
 XX  
 SQ Sequence 10 BP; 1 A; 5 C; 0 G; 4 T; 0 other;  
 XX  
 Query Match  
 Best Local Similarity 100.0%; Score 10; DB 24; Length 10;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 1 CTTTCACCT 10  
 DB 1 CTTTCACCT 10  
 XX  
 RESULT 10  
 ID AA057929/c  
 AC AA057929 standard; DNA; 11 BP.  
 XX  
 AC AA057929;  
 XX  
 DT 12-AUG-1994 (first entry)  
 XX  
 DE Oligonucleotide #1 to diagnose compulsive behaviour disorders.  
 XX  
 KW Human dopamine D2 receptor; genetic susceptibility; diagnosis;  
 KW DRD2; compulsive disorder; alcoholism; cocaine dependence;  
 KW

KW Tourette's Syndrome; attention deficit disorder; hyperactivity;  
 KW post-traumatic stress disorder; PCR amplification; RFLP;  
 KW restriction fragment length polymorphism; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN AU9331129-A.  
 XX  
 PD 06-JAN-1994.  
 XX  
 PF 11-JAN-1993; 93AU-0031129.  
 XX  
 PR 24-JUN-1992; 92US-0909282.  
 XX  
 PA (REGC) UNIV CALIFORNIA.  
 PA (TEXA) UNIV TEXAS SYSTEM.  
 XX  
 PI Blum K, Noble EP, Sheridan PJ;  
 XX  
 DR WPI; 1994-057631/08.  
 XX  
 PT Detecting a genetic potential susceptibility to a compulsive  
 PT disorder - by detecting in DNA from a subject a human dopamine D2  
 PT receptor gene allele  
 XX  
 PS Disclosure; Page 148; 165pp; English.  
 XX  
 CC Compulsive disorder susceptibility in humans can be detected  
 CC by determining the presence or absence of a particular dopamine D2  
 CC receptor allele in a DNA sample. Partic. the A1 and B1 alleles are  
 CC detected, as these alleles have been found to be present in a  
 CC majority of clinically diagnosed alcoholics and cocaine users.  
 CC Detection can be by PCR amplification (see AA057927-8 for pref.  
 CC primers) or by restriction fragment length polymorphism.  
 CC (N.B. There are no direct references to AA057929-057932 in the  
 CC specification.)  
 XX  
 SQ Sequence 11 BP; 4 A; 0 C; 6 G; 1 T; 0 other;  
 XX  
 Query Match  
 Best Local Similarity 100.0%; Score 10; DB 15; Length 11;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 1 CTTTCACCT 10  
 DB 11 CTTTCACCT 2  
 XX  
 RESULT 11  
 ID AAT18122/c  
 AC AAT18122 standard; DNA; 11 BP.  
 XX  
 AC AAT18122;  
 XX  
 DT 22-AUG-1996 (first entry)  
 XX  
 DE Human dopamine D2 receptor DRD2 intron 6 polymorphic site (3208T).  
 XX  
 KW Dopamine D2 receptor; A1 allele; B1 allele; polymerase chain reaction;  
 KW PCR amplification of specific alleles; PASA; compulsive disorder;  
 KW cocaine dependence; alcoholism; genetic susceptibility; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key  
 FH allele  
 FT 6 location/Qualifiers  
 FT /\*tag- a  
 FT /note- "nucleotides 3203-3213 of DRD2 in which  
 FT there is a T at the polymorphic position  
 FT 3208"  
 XX  
 PN US5500343-A.  
 XX

PD 19-MAR-1996.  
 XX  
 PF 07-FEB-1990; 90US-0477057.  
 XX  
 PR 24-JUN-1992; 92US-0909383.  
 PR 07-FEB-1990; 90US-0477057.  
 PR 23-JAN-1992; 92US-0826222.  
 XX  
 PA (REGC ) UNIV CALIFORNIA.  
 PA (TEXA ) UNIV TEXAS SYSTEM.  
 XX  
 PI Blum K, Noble EP, Sheridan PJ;  
 DR WPI; 1996-171043/17.  
 XX  
 PT Detecting genetic potential susceptibility to cocaine dependence or  
 PT alcoholism - by detecting human dopamine D2 receptor gene A1 or B1  
 PT allele in the subject's DNA  
 XX  
 PS Example 3; Column 45; 56pp; English.  
 XX  
 CC The dopamine D2 receptor DRD2(In6-Ex7) haplotype is comprised of  
 CC two polymorphisms that are separated by 212 bp and span the  
 CC junction of the intron 6 and exon 7 sequences. The first is a T or  
 CC G at position 3208 and the second polymorphism is a T or C at  
 CC position 3420, providing 4 possible haplotypes. Haplotype 1 is  
 CC characterised by T at position 3208 and C at position 3420.  
 CC The primers #3208 and #3420 specifically amplify a 241 bp fragment  
 CC (3433-3193+1) beginning in intron 6 and ending in exon 7 of the  
 CC dopamine D2 receptor haplotype 1 which is associated with  
 CC alcoholism. The primers are used in a claimed method for detecting  
 CC genetic potential susceptibility to alcoholism in human subjects.  
 CC In particular, amplification is carried out using the PSA  
 CC technique (i.e. PCR Amplification of Specific Alleles). In related  
 CC methods, genetic potential susceptibility to cocaine dependence can  
 CC be detected by amplifying human dopamine D2 receptor A1 and B1  
 CC alleles (primers not specified).  
 XX  
 SO Sequence 11 BP; 4 A; 0 C; 6 G; 1 T; 0 other;  
 Query Match 100.0%; Score 10; DB 17; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 4.3e+03;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 1 CTTTCACCT 10  
 Db 11 CTTTCACCT 2  
 XX  
 RESULT 12  
 AAX14846/C  
 ID AAX14846 standard; DNA; 12 BP.  
 XX  
 AC AAX14846;  
 XX  
 DT 24-MAR-1999 (first entry)  
 XX  
 DE Triple helix forming nucleotides 384-395 of 23S rRNA gene.  
 XX  
 KM Triple-helix forming region; Triplex formation; DNA detection;  
 KM identification; bacteria; oncogene; virus; ds.  
 XX  
 OS Leptospira interrogans.  
 XX  
 PN US5861244-A.  
 XX  
 PD 19-JAN-1999.  
 XX  
 PF 22-DEC-1993; 93US-0173489.  
 XX  
 PR 22-DEC-1993; 93US-0173489.  
 PR 29-OCT-1992; 92US-0968436.  
 XX

PA (PROF-) PROFILE DIAGNOSTIC SCI INC.  
 XX  
 PI Hepburn AG, Wang C;  
 XX  
 DR WPI; 1999-130384/11.  
 XX  
 PT Assay of genetic sequences based on triplex formation from double  
 PT stranded analyte - and hybrid of anchor and reporter sequences, with  
 PT reporter released if triplex formation occurs, used e.g. to identify  
 PT bacteria  
 XX  
 PS Disclosure; Columns 21-22; 168pp; English.  
 XX  
 CC The present sequence represents a potential triple-helix forming region.  
 CC It can be used to demonstrate the assay of the invention. The assay  
 CC comprises adding a sample containing double-stranded DNA test sequences,  
 CC e.g. containing the present sequence, to an aqueous medium containing at  
 CC least one complex of anchor DNA, attached to a solid support, and  
 CC reporter DNA, where either a part of the anchor DNA or reporter DNA is  
 CC designed to form a triple-strand structure with part of the test  
 CC sequence. Triplex formation results in displacement of the reporter DNA  
 CC which is detected as an indication of the presence of the DNA test  
 CC sequence. The method is used to detect DNA sequences, particularly for  
 CC identification of bacteria (by detecting genes for ribosomal RNA) in  
 CC clinical samples, but also detection of oncogenes and Hepatitis B virus.  
 XX  
 SO Sequence 12 BP; 5 A; 0 C; 6 G; 1 T; 0 other;  
 Query Match 100.0%; Score 10; DB 20; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 4.3e+03;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 1 CTTTCACCT 10  
 Db 12 CTTTCACCT 3  
 XX  
 RESULT 13  
 ABF08726/C  
 ID ABF08726 standard; DNA; 13 BP.  
 XX  
 AC ABF08726;  
 XX  
 DT 21-FEB-2002 (first entry)  
 XX  
 DE Oligonucleotide SEQ ID NO 108723 for detecting SNP TSC0027206.  
 XX  
 KM SNP: single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 KM peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 KM central nervous system; gastrointestinal; respiratory; immune; metabolic.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200177384-A2.  
 XX  
 PD 18-OCT-2001.  
 XX  
 PF 06-APR-2001; 2001WO-1B00713.  
 XX  
 PR 07-APR-2000; 2000DE-1019173.  
 XX  
 FA (EPIC-) EPIDENOMICS AG.  
 XX  
 PI Olek A, Piepenbrock C, Berlin K;  
 XX  
 DR WPI; 2001-657177/75.  
 XX  
 PT Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single nucleotide polymorphisms and cytosine  
 PT methylation status  
 XX  
 PS Claim 1; SEQ ID 108723; 29pp + Sequence Listing; German.  
 XX



CC This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a CC range of diseases including immune system, gastrointestinal, respiratory, CC central nervous system, cardiovascular and metabolic disorders. The CC oligomers are also used for detecting cell type differentiation. CC ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and CC AB100010-AB182073 represent the oligomers described in the invention. CC NOTE: The sequence data for this patent did not form part of the printed CC specification, but was obtained in electronic format from WIPO at CC ftp.wipo.int/pub/published\_pct\_sequences.

SO Sequence 13 BP; 4 A; 0 C; 5 G; 4 T; 0 other;

Query Match 100.0%; Score 10; DB 23; Length 13;  
Best Local Similarity 100.0%; Pred. No. 4.3e+03;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CTTTCACCT 10  
13 CTTTCACCT 4

Db 13 CTTTCACCT 4

RESULT 14  
ABF08727  
ID ABF08727 standard; DNA: 13 BP.  
AC ABF08727;  
DT 21-FEB-2002 (first entry)

XX oligonucleotide SEQ ID NO 108724 for detecting SNP TSC0027206.

DE SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX Homo sapiens.  
XX WO200177384-A2.  
XX 18-OCT-2001.  
XX PD 06-APR-2001; 2001WO-IB00713.  
XX PF 07-APR-2000; 2000DE-1019173.  
XX PR (EPIC-) EPIGENOMICS AG.  
XX PA Olek A, Piepenbrock C, Berlin K;  
XX PI WPI: 2001-657177/75.  
XX DR Set of oligonucleotides, useful for diagnosis and cell typing, is  
XX PT designed to detect single nucleotide polymorphisms and cytosine  
XX PT methylation status  
XX PS Claim 1; SEQ ID 108724; 29pp + Sequence listing; German.

CC This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a CC range of diseases including immune system, gastrointestinal, respiratory, CC central nervous system, cardiovascular and metabolic disorders. The CC oligomers are also used for detecting cell type differentiation. CC ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and CC AB100010-AB182073 represent the oligomers described in the invention. CC NOTE: The sequence data for this patent did not form part of the printed CC specification, but was obtained in electronic format from WIPO at CC ftp.wipo.int/pub/published\_pct\_sequences.

SO Sequence 13 BP; 4 A; 5 C; 0 G; 4 T; 0 other;

Query Match 100.0%; Score 10; DB 23; Length 13;  
Best Local Similarity 100.0%; Pred. No. 4.3e+03;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CTTTCACCT 10  
1 CTTTCACCT 10

Db 1 CTTTCACCT 10

RESULT 15  
ABH24716/C  
ID ABH24716 standard; DNA: 13 BP.  
AC ABH24716;  
DT 22-FEB-2002 (first entry)

XX oligonucleotide SEQ ID NO 224693 for detecting SNP TSC0054769.

DE SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX Homo sapiens.  
XX WO200177384-A2.  
XX 18-OCT-2001.  
XX PD 06-APR-2001; 2001WO-IB00713.  
XX PF 07-APR-2000; 2000DE-1019173.  
XX PR (EPIC-) EPIGENOMICS AG.  
XX PA Olek A, Piepenbrock C, Berlin K;  
XX PI WPI: 2001-657177/75.  
XX DR Set of oligonucleotides, useful for diagnosis and cell typing, is  
XX PT designed to detect single nucleotide polymorphisms and cytosine  
XX PT methylation status  
XX PS Claim 1; SEQ ID 224693; 29pp + Sequence listing; German.

CC This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a CC range of diseases including immune system, gastrointestinal, respiratory, CC central nervous system, cardiovascular and metabolic disorders. The CC oligomers are also used for detecting cell type differentiation. CC ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and CC AB100010-AB182073 represent the oligomers described in the invention. CC NOTE: The sequence data for this patent did not form part of the printed CC specification, but was obtained in electronic format from WIPO at CC ftp.wipo.int/pub/published\_pct\_sequences.

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OM nucleic - nucleic search, using sw model

Run on: March 19, 2003, 00:00:11 ; Search time 37 Seconds

(without alignments)  
82.886 Million cell updates/sec

Title: US-09-702-498A-33

Perfect score: 10

Sequence: 1 CTTTCACCT 10

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued\_Patents\_NA:\*  
1: /cgn2\_6/ptodata1/1na/5A\_COMB.seq:\*  
2: /cgn2\_6/ptodata1/1na/5B\_COMB.seq:\*  
3: /cgn2\_6/ptodata1/1na/6A\_COMB.seq:\*  
4: /cgn2\_6/ptodata1/1na/6B\_COMB.seq:\*  
5: /cgn2\_6/ptodata1/1na/PCTUS\_COMB.seq:\*  
6: /cgn2\_6/ptodata1/1na/backfile1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	10	100.0	11	1	US-07-909-383-1
C 2	10	100.0	12	2	US-08-173-489C-233
C 3	10	100.0	19	3	US-08-777-266A-95
C 4	10	100.0	19	4	US-09-326-186B-95
C 5	10	100.0	22	3	US-08-777-266A-94
C 6	10	100.0	22	4	US-09-326-186B-94
C 7	10	100.0	23	1	US-07-952-442-7
C 8	10	100.0	23	1	US-08-269-766-7
C 9	10	100.0	23	1	US-08-319-545A-7
C 10	10	100.0	23	3	US-09-092-988-7
C 11	10	100.0	23	3	US-09-106-216-7
C 12	10	100.0	23	4	US-09-429-034-7
C 13	10	100.0	24	3	US-08-777-266A-93
C 14	10	100.0	24	4	US-09-326-186B-93
C 15	10	100.0	124	4	US-08-205-697A-39
C 16	10	100.0	124	4	US-08-702-525-39
C 17	10	100.0	124	5	PCT-US95-02576-39
C 18	10	100.0	333	3	US-09-009-913-15
C 19	10	100.0	337	3	US-08-702-652-40
C 20	10	100.0	377	6	5168053-1
C 21	10	100.0	397	4	US-08-636-597-2
C 22	10	100.0	438	4	US-09-232-063-2
C 23	10	100.0	440	4	US-09-328-986-56
C 24	10	100.0	440	4	US-09-397-787-321
C 25	10	100.0	584	4	US-09-328-111-83
C 26	10	100.0	616	4	US-09-328-111-574
C 27	10	100.0	650	4	US-09-328-111-189

28	10	100.0	650	4	US-09-404-879A-262	Sequence 262, App
29	10	100.0	676	4	US-09-221-017B-72	Sequence 72, App1
30	10	100.0	709	1	US-08-469-667-12	Sequence 12, App1
31	10	100.0	709	4	US-09-224-110-12	Sequence 12, App1
32	10	100.0	709	5	PCT-US95-07289-12	Sequence 12, App1
33	10	100.0	726	3	US-08-660-645A-11	Sequence 11, App1
34	10	100.0	726	3	US-09-298-718-11	Sequence 11, App1
35	10	100.0	726	4	US-09-546-969-11	Sequence 11, App1
36	10	100.0	726	4	US-08-980-832-28	Sequence 11, App1
37	10	100.0	747	4	US-09-134-001C-1462	Sequence 1462, App
C 38	10	100.0	771	1	US-08-253-155A-17	Sequence 17, App1
C 39	10	100.0	778	2	US-08-781-560-2	Sequence 2, App1
C 40	10	100.0	1013	6	5242798-8	Sequence 2, App1
C 41	10	100.0	1036	3	US-09-267-031-9	Sequence 9, App1
C 42	10	100.0	1037	4	US-09-535-008-57	Sequence 57, App1
C 43	10	100.0	1103	4	US-08-936-165A-128	Sequence 128, App
C 44	10	100.0	1120	2	US-08-456-104-1	Sequence 1, App1
C 45	10	100.0	1120	2	US-08-101-624-1	Sequence 1, App1

## ALIGNMENTS

RESULT 1  
US-07-909-383-1/c  
Sequence 1, Application US/07909383  
Patent No. 5500343  
GENERAL INFORMATION:  
APPLICANT: BILM, KENNETH  
APPLICANT: NOBLE, E.P.  
TITLE OF INVENTION: ALLELIC ASSOCIATION OF THE HUMAN  
TITLE OF INVENTION: DOPAMINE (D2) RECEPTOR GENE IN  
TITLE OF INVENTION: COMPULSIVE DISORDERS  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: ARNOLD, WHITE & DURKEE  
STREET: P.O. BOX 4433  
CITY: HOUSTON  
STATE: TEXAS  
COUNTRY: USA  
ZIP: 77210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: FLOPPY DISK  
COMPUTER: IBM PC COMPATIBLE  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WORDPERFECT 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/909,383  
FILING DATE: 19920624  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: HODGINS, DANIEL S.  
REGISTRATION NUMBER: 31,026  
REFERENCE/DOCKET NUMBER: UTSK:187  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 512-320-7200  
TELEFAX: 512-474-7577  
TELEX: NOT APPLICABLE  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 11 base pairs  
TYPE: NUCLEIC ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-07-909-383-1  
Query Match 100.0%; Score 10; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 66+02;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
1 CTTTCACCT 10  
|||||||

Db 11 CTTACACCT 2

## RESULT 2

US-08-173-489C-233/C  
Sequence 233, Application US/08173489C  
Patent No. 3861244  
GENERAL INFORMATION:  
APPLICANT: WANG, C. -G.  
APPLICANT: HEPBURN, A. G.  
TITLE OF INVENTION: GENETIC SEQUENCE ASSAY USING DNA  
TITLE OF INVENTION: TRIPLE-STRAND FORMATION.  
NUMBER OF SEQUENCES: 365  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: PROFILE DIAGNOSTIC SCIENCES, INC.,  
STREET: 510 EAST 73RD STREET,  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10021.  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44MB storage  
COMPUTER: IBM PC/XT/AT  
OPERATING SYSTEM: MS-DOS version 6.2  
SOFTWARE: Wordperfect Version 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/173,489C  
FILING DATE: 22 DEC 1993  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/968,436  
FILING DATE: 29 OCT 1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Handelman, Joseph H.  
REGISTRATION NUMBER: 26,179  
REFERENCE/DOCKET NUMBER: U9518-6  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (attorney) (212) 708-1880  
TELEFAX: (attorney) (212) 246-8959  
INFORMATION FOR SEQ ID NO: 233:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 12 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double stranded  
TOPOLOGY: linear  
MOLECULE TYPE: genomic DNA  
DESCRIPTION: 23S rRNA gene from Leptospira  
DESCRIPTION: Interrogans (Accession # X14249) nucleotides  
DESCRIPTION: 384 to 395  
HYPOTHETICAL: no  
ANTI-SENSE: no  
ORIGINAL SOURCE:  
ORGANISM: Leptospira interrogans serovar canicola  
STRAIN: moulton  
PUBLICATION INFORMATION:  
AUTHORS: Fukunaga, M, Horie, I, Mituchi, I.  
TITLE: Nucleotide sequence of a 23S  
TITLE: ribosomal RNA gene for Leptospira interrogans  
JOURNAL: serovar canicola strain moulton  
VOLUME: 17  
PAGES: 2123-2123  
DATE: 1989  
RELEVANT RESIDUES IN SEQ ID NO: 233 :FROM 1 TO 12  
US-08-173-489C-233

## Query Match

Best Local Similarity 100.0%; Score 10; DB 2; Length 12;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTACACCT 10  
|||||  
Db 12 CTTACACCT 3

## RESULT 3

US-08-777-266A-95  
Sequence 95, Application US/08777266A  
Patent No. 6077833  
GENERAL INFORMATION:  
APPLICANT: Clarence Frank Bennett  
APPLICANT: Timothy A. Vickers  
TITLE OF INVENTION: Oligonucleotide Compositions and  
TITLE OF INVENTION: Methods for the Modulation of the Expression of B7 Prot  
NUMBER OF SEQUENCES: 125  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Law Offices of Jane Massey Licata  
STREET: 210 Lake Drive East, Suite 201  
CITY: Cherry Hill  
STATE: NJ  
COUNTRY: USA  
ZIP: 08002.  
COMPUTER READABLE FORM:  
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE  
COMPUTER: IBM PS/2  
OPERATING SYSTEM: PC-DOS  
SOFTWARE: WORDPERFECT 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/777,266A  
FILING DATE: December 31, 1996  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Jane Massey Licata  
REGISTRATION NUMBER: 32,257  
REFERENCE/DOCKET NUMBER: ISPH-0201  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (609) 779-2400  
TELEFAX: (609) 779-8488  
INFORMATION FOR SEQ ID NO: 95:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 19  
TYPE: Nucleic Acid  
STRANDEDNESS: Single  
TOPOLOGY: Linear  
ANTI-SENSE: Yes  
US-08-777-266A-95

## Query Match

Best Local Similarity 100.0%; Score 10; DB 3; Length 19;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTACACCT 10  
|||||  
Db 7 CTTACACCT 16

## RESULT 4

US-09-326-186B-95  
Sequence 95, Application US/09326186B  
Patent No. 6319906  
GENERAL INFORMATION:  
APPLICANT: Bennett, Clarence Frank  
APPLICANT: Vickers, Timothy A.  
TITLE OF INVENTION: Oligonucleotide Compositions and Methods for the  
TITLE OF INVENTION: Modulation of the Expression of B7 Protein  
FILE REFERENCE: ISPH-0376  
CURRENT APPLICATION NUMBER: US/09/326,186B  
CURRENT FILING DATE: 1999-06-04  
PRIOR APPLICATION NUMBER: 08/777,266  
PRIOR FILING DATE: 1996-12-31  
NUMBER OF SEQ ID NOS: 226  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 95

LENGTH: 19  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthetic  
US-09-326-186B-95

Query Match  
Best Local Similarity 100.0%; Score 10; DB 4; Length 19;  
Pred. No. 6.1e+02;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTTCACCT 10  
Db 7 CTTTCACCT 16

RESULT 5  
US-08-777-266A-94  
Sequence 94, Application US/08777266A  
Patent No. 6077833  
GENERAL INFORMATION:  
APPLICANT: Clarence Frank Bennett  
APPLICANT: Timothy A. Vickers  
TITLE OF INVENTION: Oligonucleotide Compositions and  
TITLE OF INVENTION: Methods for the Modulation of the Expression of B7 Proteins  
NUMBER OF SEQUENCES: 125  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Law Offices of Jane Massey Licata  
STREET: 210 Lake Drive East, Suite 201  
CITY: Cherry Hill  
STATE: NJ  
COUNTRY: USA  
ZIP: 08002  
COMPUTER READABLE FORM:  
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE  
COMPUTER: IBM PS/2  
OPERATING SYSTEM: PC-DOS  
SOFTWARE: WORDPERFECT 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/777,266A  
FILING DATE: December 31, 1996  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Jane Massey Licata  
REGISTRATION NUMBER: 32,257  
REFERENCE/DOCKET NUMBER: ISPH-0201  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (609) 779-2400  
TELEFAX: (609) 779-8488  
INFORMATION FOR SEQ ID NO: 94:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 22  
TYPE: Nucleic Acid  
STRANDEDNESS: Single  
TOPOLOGY: Linear  
ANTI-SENSE: Yes  
US-08-777-266A-94

Query Match  
Best Local Similarity 100.0%; Score 10; DB 3; Length 22;  
Pred. No. 6.2e+02;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTTCACCT 10  
Db 10 CTTTCACCT 19

RESULT 6  
US-09-326-186B-94  
Sequence 94, Application US/09326186B

Patent No. 6319906  
GENERAL INFORMATION:  
APPLICANT: Bennett, Clarence Frank  
APPLICANT: Vickers, Timothy A.  
TITLE OF INVENTION: Oligonucleotide Compositions and Methods for the  
TITLE OF INVENTION: Modulation of the Expression of B7 Protein  
FILE REFERENCE: ISPH-0376  
CURRENT APPLICATION NUMBER: US/09/326,186B  
CURRENT FILING DATE: 1999-06-04  
PRIOR APPLICATION NUMBER: 08/777,266  
PRIOR FILING DATE: 1996-12-31  
NUMBER OF SEQ ID NOS: 226  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 94  
LENGTH: 22  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthetic  
US-09-326-186B-94

Query Match  
Best Local Similarity 100.0%; Score 10; DB 4; Length 22;  
Pred. No. 6.2e+02;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTTCACCT 10  
Db 10 CTTTCACCT 19

RESULT 7  
US-07-952-442-7  
Sequence 7, Application US/07952442  
Patent No. 5374525  
GENERAL INFORMATION:  
APPLICANT: Lalouel, Jean-Marc  
APPLICANT: Jeunemaitre, Xavier  
APPLICANT: Lifton, Richard P.  
APPLICANT: Soubrier, Florent  
APPLICANT: Kotelevtsev, Youri  
TITLE OF INVENTION: Angiotensinogen Gene Variants and  
TITLE OF INVENTION: Predisposition to Essential Hypertension  
NUMBER OF SEQUENCES: 22  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Venable, Baetjer, Howard & Civiletti  
STREET: 1201 New York Avenue N.W., Suite 1000  
CITY: Washington  
STATE: DC  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/952,442  
FILING DATE: 19920930  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Immen, Jeffrey L.  
REGISTRATION NUMBER: 28,957  
REFERENCE/DOCKET NUMBER: 19780-104502  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-962-4810  
TELEX: 202-962-8300  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 23 base pairs  
TYPE: NUCLEIC ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)

HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
US-07-952-442-7

Query Match  
Best Local Similarity 100.0%; Score 10; DB 1; Length 23;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTTCACCT 10  
13 CTTTCACCT 22

RESULT 8  
US-08-269-766-7  
Sequence 7, Application US/08269766  
Patent No. 5589584  
GENERAL INFORMATION:

APPLICANT: Lalouel, Jean-Marc  
APPLICANT: Jeunemaitre, Xavier  
APPLICANT: Lifton, Richard P.  
APPLICANT: Soubrier, Florent  
APPLICANT: Kotelevtsev, Youri  
APPLICANT: Corvol, Pierre  
TITLE OF INVENTION: Angiotensinogen Gene Variants and  
TITLE OF INVENTION: Predisposition to Essential Hypertension  
NUMBER OF SEQUENCES: 22  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Venable, Baetjer, Howard & Civiletti  
STREET: 1201 New York Avenue N.W., Suite 1000  
CITY: Washington  
STATE: DC  
ZIP: 20005

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC Compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/269,766  
FILING DATE: 01-JUL-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/952,442  
FILING DATE: 30-SEP-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Ihnen, Jeffrey L.  
REGISTRATION NUMBER: 28,957  
REFERENCE/DOCKET NUMBER: 19780-104502  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-962-4810  
TELEX: 202-962-8300

INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 23 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
US-08-269-766-7

Query Match  
Best Local Similarity 100.0%; Score 10; DB 1; Length 23;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTTCACCT 10  
13 CTTTCACCT 22

DB 13 CTTTCACCT 22

RESULT 9  
US-08-319-545A-7  
Sequence 7, Application US/08319545A  
Patent No. 5763168  
GENERAL INFORMATION:

APPLICANT: Lalouel, Jean-Marc  
APPLICANT: Jeunemaitre, Xavier  
APPLICANT: Lifton, Richard P.  
APPLICANT: Soubrier, Florent  
APPLICANT: Kotelevtsev, Youri  
APPLICANT: Corvol, Pierre  
TITLE OF INVENTION: Method to Determine Predisposition  
TITLE OF INVENTION: to Hypertension  
NUMBER OF SEQUENCES: 22  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Venable, Baetjer, Howard & Civiletti  
STREET: 1201 New York Avenue N.W., Suite 1000  
CITY: Washington  
STATE: DC  
ZIP: 20005

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC Compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Wordperfect 5.1/5.2 Windows  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/319,545A  
FILING DATE: 7-OCT-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/952,442  
FILING DATE: 30-SEP-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Ihnen, Jeffrey L.  
REGISTRATION NUMBER: 28,957  
REFERENCE/DOCKET NUMBER: 19780-104502-2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-962-4810  
TELEX: 202-962-8300

INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 23 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
US-08-319-545A-7

Query Match  
Best Local Similarity 100.0%; Score 10; DB 1; Length 23;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTTCACCT 10  
13 CTTTCACCT 22

RESULT 10  
US-09-092-988-7  
Sequence 7, Application US/09092988  
Patent No. 5998145  
GENERAL INFORMATION:

APPLICANT: Lalouel, Jean-Marc  
APPLICANT: Jeunemaitre, Xavier  
APPLICANT: Lifton, Richard P.  
APPLICANT: Soubrier, Florent

APPLICANT: Kotelevtsev, Yuri  
APPLICANT: Corvol, Pierre  
TITLE OF INVENTION: Method to Determine Predisposition  
TITLE OF INVENTION: to Hypertension  
NUMBER OF SEQUENCES: 22  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Venable, Baetjer, Howard & Civiletti  
STREET: 1201 New York Avenue N.W., Suite 1000  
CITY: Washington  
STATE: DC  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Wordperfect 5.1/5.2 Windows  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/092,988  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/319,545  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Ihnen, Jeffrey L.  
REGISTRATION NUMBER: 28,957  
REFERENCE/DOCKET NUMBER: 19780-104502-2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-962-4810  
TELEX: 202-962-8300  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 23 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
US-09-092-988-7

Query Match 100.0%; Score 10; DB 2; Length 23;  
Best Local Similarity 100.0%; Pred No. 6.2e+02;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTTCACCTT 10  
DB 13 CTTTCACCTT 22

RESULT 11  
US-09-106-216-7  
Sequence 7, Application US/09106216  
Patent No. 6153386  
GENERAL INFORMATION:  
APPLICANT: Lalouel, Jean-Marc  
APPLICANT: Jeunemaitre, Xavier  
APPLICANT: Lofton, Richard P.  
APPLICANT: Soubrier, Florent  
APPLICANT: Kotelevtsev, Yuri  
APPLICANT: Corvol, Pierre  
TITLE OF INVENTION: Method to Determine Predisposition to  
TITLE OF INVENTION: Hypertension  
NUMBER OF SEQUENCES: 58  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Rothwell, Figg, Ernst & Kurz  
STREET: 555 Thirteenth Street N.W., Suite 701-E  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20004

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/106,216  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 09/  
FILING DATE: 08-JUN-1998  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/319,545  
FILING DATE: 07-OCT-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/952,545  
FILING DATE: 30-SEP-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Ihnen, Jeffrey L.  
REGISTRATION NUMBER: 28,957  
REFERENCE/DOCKET NUMBER: 2323-124  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-783-6040  
TELEFAX: 202-783-6031  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 23 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "primer"  
US-09-106-216-7

Query Match 100.0%; Score 10; DB 3; Length 23;  
Best Local Similarity 100.0%; Pred No. 6.2e+02;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTTCACCTT 10  
DB 13 CTTTCACCTT 22

RESULT 12  
US-09-429-034-7  
Sequence 7, Application US/09429034  
Patent No. 6165727  
GENERAL INFORMATION:  
APPLICANT: Lalouel, Jean-Marc  
APPLICANT: Jeunemaitre, Xavier  
APPLICANT: Lofton, Richard P.  
APPLICANT: Soubrier, Florent  
APPLICANT: Kotelevtsev, Yuri  
APPLICANT: Corvol, Pierre  
TITLE OF INVENTION: Method to Determine Predisposition  
TITLE OF INVENTION: to Hypertension  
NUMBER OF SEQUENCES: 22  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Venable, Baetjer, Howard & Civiletti  
STREET: 1201 New York Avenue N.W., Suite 1000  
CITY: Washington  
STATE: DC  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Wordperfect 5.1/5.2 Windows  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/429,034  
FILING DATE:  
CLASSIFICATION:

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/319,545  
FILING DATE: 7-OCT-1994  
APPLICATION NUMBER: US 07/952,442  
FILING DATE: 30-SEP-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Ihnen, Jeffrey L.  
REGISTRATION NUMBER: 28,957  
REFERENCE/DOCKET NUMBER: 19780-104502-2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-962-4810  
TELEX: 202-962-8300  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 23 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
US-09-429-034-7

Query Match  
Best Local Similarity 100.0%; Score 10; DB 4; Length 23;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTTCACCT 10  
DB 13 CTTTCACCT 22

RESULT 13  
US-08-777-266A-93  
Sequence 93, Application US/08777266A  
Patent No. 6077833  
GENERAL INFORMATION:  
APPLICANT: Clarence Frank Bennett  
APPLICANT: Timothy A. Vickers  
TITLE OF INVENTION: Oligonucleotide Compositions and  
TITLE OF INVENTION: Methods for the Modulation of B7 Proteins  
NUMBER OF SEQUENCES: 125  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Law Offices of Jane Massey Licata  
STREET: 210 Lake Drive East, Suite 201  
CITY: Cherry Hill  
STATE: NJ  
COUNTRY: USA  
ZIP: 08002  
COMPUTER READABLE FORM:  
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE  
COMPUTER: IBM PS/2  
OPERATING SYSTEM: PC-DOS  
SOFTWARE: WORDPERFECT 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/777,266A  
FILING DATE: December 31, 1996  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Jane Massey Licata  
REGISTRATION NUMBER: 32,257  
REFERENCE/DOCKET NUMBER: ISPH-0201  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (609) 779-2400  
TELEFAX: (609) 779-8488  
INFORMATION FOR SEQ ID NO: 93:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 24

TYPE: Nucleic Acid  
STRANDEDNESS: Single  
TOPOLOGY: Linear  
ANTI-SENSE: Yes  
US-08-777-266A-93

Query Match  
Best Local Similarity 100.0%; Score 10; DB 3; Length 24;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTTCACCT 10  
DB 12 CTTTCACCT 21

RESULT 14  
US-09-326-186B-93  
Sequence 93, Application US/09326186B  
Patent No. 6319906  
GENERAL INFORMATION:  
APPLICANT: Bennett, Clarence Frank  
APPLICANT: Vickers, Timothy A.  
TITLE OF INVENTION: Oligonucleotide Compositions and Methods for the  
TITLE OF INVENTION: Modulation of the Expression of B7 Protein  
FILE REFERENCE: ISPH-0376  
CURRENT APPLICATION NUMBER: US/09/326,186B  
CURRENT FILING DATE: 1999-06-04  
PRIOR APPLICATION NUMBER: 08/777,266  
NUMBER OF SEQ ID NOS: 226  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 93  
LENGTH: 24  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthetic  
US-09-326-186B-93

Query Match  
Best Local Similarity 100.0%; Score 10; DB 4; Length 24;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTTCACCT 10  
DB 12 CTTTCACCT 21

RESULT 15  
US-08-205-697A-39/C  
Sequence 39, Application US/08205697A  
Patent No. 6218510  
GENERAL INFORMATION:  
APPLICANT: Sharpe, Arlene H.  
APPLICANT: Bortelle, Francescopaulo  
APPLICANT: Freeman, Gordon J.  
APPLICANT: Nadler, Lee M.  
TITLE OF INVENTION: No. 6218510el Forms of T Cell Costimulatory Molecules  
TITLE OF INVENTION: and Uses Therefor  
NUMBER OF SEQUENCES: 61  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LAHIVE & COCKFIELD  
STREET: 60 State Street, suite 510  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109-1875  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII Text  
CURRENT APPLICATION DATA:



APPLICATION NUMBER: US/08/205,697A  
FILING DATE: 02-Mar-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Mandragouras, Amy E.  
REGISTRATION NUMBER: 36,207  
REFERENCE/DOCKET NUMBER: BMT-120  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617)227-7400  
TELEFAX: (617)227-5941  
INFORMATION FOR SEQ ID NO: 39:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 124 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 107..124  
US-08-205-697A-39

Query Match 100.0%; Score 10; DB 4; Length 124;  
Best Local Similarity 100.0%; Pred. No. 6.9e+02;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTTCACCT 10  
|||||  
Db 13 CTTTCACCT 4

Search completed: March 19, 2003, 01:26:20  
Job time : 39 secs

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GenCore version 5.1.4-p5\_4578  
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## OM nucleic - nucleic search, using sw model

Run on: March 19, 2003, 00:40:46 ; Search time 51.5 Seconds

(without alignments)  
136.284 Million cell updates/sec

Title: US-09-702-498A-33

Perfect score: 10

Sequence: 1 CTTTCACCCCT 10

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 501302 seqs, 350932545 residues

Total number of hits satisfying chosen parameters: 1002604

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

## Database :

Published Applications NA:\*

- 1: /cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq:\*
- 2: /cgn2\_6/ptodata/1/pubpna/PCT\_NEW\_PUB.seq:\*
- 3: /cgn2\_6/ptodata/1/pubpna/US06\_NEW\_PUB.seq:\*
- 4: /cgn2\_6/ptodata/1/pubpna/US06\_PUBCOMB.seq:\*
- 5: /cgn2\_6/ptodata/1/pubpna/US07\_NEW\_PUB.seq:\*
- 6: /cgn2\_6/ptodata/1/pubpna/PCTUS\_PUBCOMB.seq:\*
- 7: /cgn2\_6/ptodata/1/pubpna/US08\_NEW\_PUB.seq:\*
- 8: /cgn2\_6/ptodata/1/pubpna/US08\_PUBCOMB.seq:\*
- 9: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq:\*
- 10: /cgn2\_6/ptodata/1/pubpna/US09\_PUBCOMB.seq:\*
- 11: /cgn2\_6/ptodata/1/pubpna/US10\_NEW\_PUB.seq:\*
- 12: /cgn2\_6/ptodata/1/pubpna/US10\_PUBCOMB.seq:\*
- 13: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq:\*
- 14: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	100.0	10	9	US-09-966-277-63
2	100.0	10	9	US-09-966-930-63
3	100.0	10	10	US-09-823-699-1
4	100.0	21	10	US-09-972-331-21
5	100.0	30	9	US-09-988-115A-43
6	100.0	47	9	US-09-966-277-43
7	100.0	47	9	US-09-966-277-44
8	100.0	47	9	US-09-966-930-43
9	100.0	47	9	US-09-966-930-44
10	100.0	63	10	US-09-823-699-10
11	100.0	69	10	US-09-471-840-2
12	100.0	69	10	US-09-471-840-4
13	100.0	69	10	US-09-728-207-2
14	100.0	69	10	US-09-728-207-4
15	100.0	69	10	US-09-070-938-2
16	100.0	72	9	US-09-966-277-34
17	100.0	72	9	US-09-966-277-51
18	100.0	72	9	US-09-966-277-52
19	100.0	72	9	US-09-966-930-34

C 20	10	100.0	72	9	US-09-966-930-51	Sequence 51, Appl
21	10	100.0	72	9	US-09-966-930-52	Sequence 52, Appl
22	10	100.0	72	10	US-09-843-922-3	Sequence 3, Appl
C 23	10	100.0	74	9	US-09-966-277-31	Sequence 31, Appl
24	10	100.0	74	9	US-09-966-277-32	Sequence 32, Appl
C 25	10	100.0	74	9	US-09-966-930-31	Sequence 31, Appl
26	10	100.0	74	9	US-09-966-930-32	Sequence 32, Appl
27	10	100.0	80	9	US-09-966-277-18	Sequence 18, Appl
28	10	100.0	80	9	US-09-966-930-18	Sequence 18, Appl
C 29	10	100.0	112	10	US-09-783-590-8499	Sequence 8499, Ap
C 30	10	100.0	114	10	US-09-864-761-28324	Sequence 28324, A
C 31	10	100.0	116	10	US-09-864-761-24131	Sequence 24131, A
C 32	10	100.0	117	10	US-09-864-761-17517	Sequence 17517, A
C 33	10	100.0	124	9	US-09-962-969-39	Sequence 39, Appl
C 34	10	100.0	124	10	US-09-837-867A-39	Sequence 39, Appl
C 35	10	100.0	130	10	US-09-764-846-334	Sequence 334, Ap
C 36	10	100.0	132	10	US-09-869-373-1040	Sequence 1040, Ap
C 37	10	100.0	140	10	US-09-923-876-3943	Sequence 3943, Ap
C 38	10	100.0	143	10	US-09-783-590-7779	Sequence 7779, Ap
C 39	10	100.0	148	10	US-09-864-761-23518	Sequence 23518, A
C 40	10	100.0	165	9	US-10-046-935-156	Sequence 156, Ap
C 41	10	100.0	165	9	US-09-878-178-156	Sequence 156, Ap
C 42	10	100.0	165	10	US-09-864-761-30761	Sequence 30761, A
C 43	10	100.0	165	10	US-09-878-574-11498	Sequence 11498, A
C 44	10	100.0	174	10	US-09-783-590-6678	Sequence 6678, Ap
C 45	10	100.0	180	10	US-09-983-965-2379	Sequence 2379, Ap

## ALIGNMENTS

RESULT 1  
US-09-966-277-63  
Sequence 63, Application US/09966277  
Patent No. US20020169306A1

GENERAL INFORMATION:  
APPLICANT: KITAZATO, Kaio  
APPLICANT: SHU, Tsugumine  
APPLICANT: KUMA, Hidekazu  
APPLICANT: UEDA, Yasuji  
APPLICANT: ASAKAWA, Makoto  
APPLICANT: HASEGAWA, Mamoru  
APPLICANT: IIDA, Akihito  
APPLICANT: HIRATA, Takahiro  
APPLICANT: TOKUSUMI, Tsuyoshi  
APPLICANT: INOUE, Makoto

TITLE OF INVENTION: ENVELOPE GENE-DEFICIENT PARAMYXOVIRUS  
TITLE OF INVENTION: VECTOR  
FILE REFERENCE: 50026/028001  
CURRENT APPLICATION NUMBER: US/09/966, 277  
CURRENT FILING DATE: 2001-09-27  
PRIOR APPLICATION NUMBER: PCT/JP00/03195  
PRIOR FILING DATE: 2000-05-18  
PRIOR APPLICATION NUMBER: JP 2001/283451  
PRIOR FILING DATE: 2001-09-18  
PRIOR APPLICATION NUMBER: JP 11/200739  
PRIOR FILING DATE: 1999-05-18  
NUMBER OF SEQ ID NOS: 64  
SOFTWARE: PASTSEQ for Windows Version 4.0  
SEQ ID NO 63  
LENGTH: 10  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Artificially Synthesized Sequence  
US-09-966-277-63

Query Match 100.0%; Score 10; DB 9; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Query 1 CTTTCACCCCT 10

Db 1 CTTTCACCCCT 10

## RESULT 2

US-09-966-930-63  
; Sequence 63, Application US/09966930  
; Publication No. US20030022376A1  
; GENERAL INFORMATION:  
; APPLICANT: KITAZATO, Kaio  
; APPLICANT: SHU, Tsugumine  
; APPLICANT: KUMA, Hidekazu  
; APPLICANT: UEDA, Yasuji  
; APPLICANT: ASAKAWA, Makoto  
; APPLICANT: HASEGAWA, Mamoru  
; APPLICANT: IIDA, Akihito  
; APPLICANT: HIRATA, Takahito  
; APPLICANT: INOUE, Makoto  
; TITLE OF INVENTION: PARAMYOXIVIRUS-DERIVED RNP  
; FILE REFERENCE: 50026/029001  
; CURRENT APPLICATION NUMBER: US/09/966,930  
; CURRENT FILING DATE: 2001-09-27  
; PRIOR APPLICATION NUMBER: PCT/JP00/03194  
; PRIOR FILING DATE: 2000-05-18  
; PRIOR APPLICATION NUMBER: JP 2001/283451  
; PRIOR FILING DATE: 2001-09-18  
; PRIOR APPLICATION NUMBER: JP 11/200740  
; PRIOR FILING DATE: 1999-05-18  
; NUMBER OF SEQ ID NOS: 64  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 63  
; LENGTH: 10  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Artificially Synthesized Sequence  
US-09-966-930-63

## Query Match

Best Local Similarity 100.0%; Score 10; DB 9; Length 10;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTTCACCCCT 10  
Db 1 CTTTCACCCCT 10

## RESULT 3

US-09-823-699-1  
; Sequence 1, Application US/09823699  
; Patent No. US20020002143A1  
; GENERAL INFORMATION:  
; APPLICANT: Kano, Munehide  
; APPLICANT: Matano, Tetsuro  
; APPLICANT: Kato, Atsushi  
; APPLICANT: Nagai, Yoshiyuki  
; APPLICANT: Hasegawa, Mamoru  
; TITLE OF INVENTION: AIDS Virus Vaccines Using Sendai Virus  
; FILE REFERENCE: 50026/022002  
; CURRENT APPLICATION NUMBER: US/09/823,699  
; CURRENT FILING DATE: 2001-03-30  
; PRIOR APPLICATION NUMBER: US 60/193,127  
; PRIOR FILING DATE: 2000-03-30  
; NUMBER OF SEQ ID NOS: 18  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 10  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: artificially synthesized sequence  
US-09-823-699-1

Query Match 100.0%; Score 10; DB 10; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTTCACCCCT 10  
Db 1 CTTTCACCCCT 10

## RESULT 4

US-09-972-331-21/C  
; Sequence 21, Application US/09972331  
; Patent No. US20020091083A1  
; GENERAL INFORMATION:  
; APPLICANT: HIGASHI, KIYOSHI  
; APPLICANT: KOMATSU, KENGO  
; TITLE OF INVENTION: DNA-BINDING PROTEIN YB-1-CONTAINING  
; FILE REFERENCE: 7372/72170  
; CURRENT APPLICATION NUMBER: US/09/972,331  
; CURRENT FILING DATE: 2001-12-28  
; PRIOR APPLICATION NUMBER: JP 2000/310624  
; PRIOR FILING DATE: 2000-10-11  
; NUMBER OF SEQ ID NOS: 26  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 21  
; LENGTH: 21  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: DESIGNED OLIGONUCLEOTIDE PRIMER TO SYNTHESIZE  
US-09-972-331-21

## Query Match

Best Local Similarity 100.0%; Score 10; DB 10; Length 21;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTTCACCCCT 10  
Db 11 CTTTCACCCCT 2

## RESULT 5

US-09-988-115A-43  
; Sequence 43, Application US/09988115A  
; Publication No. US20030037347A1  
; GENERAL INFORMATION:  
; APPLICANT: Rodi, James M.  
; APPLICANT: Goldsby, Richard A.  
; APPLICANT: Ferguson, Stacy E.  
; APPLICANT: Kuroiwa, Yoshima  
; APPLICANT: Tomizuka, Kazuma  
; APPLICANT: Ishida, Isao  
; TITLE OF INVENTION: Expression of Xenogenous (Human)  
; FILE REFERENCE: 50195/008003  
; CURRENT APPLICATION NUMBER: US/09/988,115A  
; CURRENT FILING DATE: 2002-08-09  
; PRIOR APPLICATION NUMBER: US 60/311,625  
; PRIOR FILING DATE: 2001-08-09  
; PRIOR APPLICATION NUMBER: US 60/256,458  
; PRIOR FILING DATE: 2000-12-20  
; PRIOR APPLICATION NUMBER: US 09/114,185  
; PRIOR FILING DATE: 2000-11-17  
; PRIOR APPLICATION NUMBER: US 60/166,410  
; PRIOR FILING DATE: 1999-11-19  
; NUMBER OF SEQ ID NOS: 68  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 43  
; LENGTH: 30  
; TYPE: DNA

```

; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Primer
US-09-988-115A-43

Query Match
Best Local Similarity 100.0%; Score 10; DB 9; Length 30;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTTCACCT 10
DB 11 CTTTCACCT 20

RESULT 6
US-09-966-277-43/c
; Sequence 43, Application US/09966277
; Patent No. US20020169306A1
; GENERAL INFORMATION:
; APPLICANT: KITAZATO, Kaito
; APPLICANT: SHU, Tsugumine
; APPLICANT: KUMA, Hidekazu
; APPLICANT: UEDA, Yasuji
; APPLICANT: ASAKAWA, Makoto
; APPLICANT: HASEGAWA, Mamoru
; APPLICANT: IIDA, Akihiro
; APPLICANT: HIRATA, Takahiro
; APPLICANT: TOKUSUMI, Tsuyoshi
; APPLICANT: INOUE, Makoto
; TITLE OF INVENTION: ENVELOPE GENE-DEFICIENT PARAMYXOVIRUS
; FILE REFERENCE: 50026/028001
; CURRENT FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: US/09/966,277
; PRIOR FILING DATE: 2000-05-18
; PRIOR APPLICATION NUMBER: PCT/JP00/03195
; PRIOR FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: JP 2001/283451
; PRIOR FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: JP 11/200739
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 43
; LENGTH: 47
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificially Synthesized Sequence
US-09-966-277-43

Query Match
Best Local Similarity 100.0%; Score 10; DB 9; Length 47;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTTCACCT 10
DB 13 CTTTCACCT 4

RESULT 7
US-09-966-277-44
; Sequence 44, Application US/09966277
; Patent No. US20020169306A1
; GENERAL INFORMATION:
; APPLICANT: KITAZATO, Kaito
; APPLICANT: SHU, Tsugumine
; APPLICANT: KUMA, Hidekazu
; APPLICANT: UEDA, Yasuji
; APPLICANT: ASAKAWA, Makoto
; APPLICANT: HASEGAWA, Mamoru
; APPLICANT: IIDA, Akihiro
; APPLICANT: HIRATA, Takahiro
; APPLICANT: TOKUSUMI, Tsuyoshi
```

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; APPLICANT: HIRATA, Takahiro
; APPLICANT: TOKUSUMI, Tsuyoshi
; APPLICANT: INOUE, Makoto
; TITLE OF INVENTION: ENVELOPE GENE-DEFICIENT PARAMYXOVIRUS
; FILE REFERENCE: 50026/028001
; CURRENT FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: US/09/966,277
; PRIOR FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: PCT/JP00/03195
; PRIOR FILING DATE: 2000-05-18
; PRIOR APPLICATION NUMBER: JP 2001/283451
; PRIOR FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: JP 11/200739
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 44
; LENGTH: 47
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificially Synthesized Sequence
US-09-966-277-44

Query Match
Best Local Similarity 100.0%; Score 10; DB 9; Length 47;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTTCACCT 10
DB 35 CTTTCACCT 44

RESULT 8
US-09-966-930-43/c
; Sequence 43, Application US/09966930
; Publication No. US20030022376A1
; GENERAL INFORMATION:
; APPLICANT: KITAZATO, Kaito
; APPLICANT: SHU, Tsugumine
; APPLICANT: KUMA, Hidekazu
; APPLICANT: UEDA, Yasuji
; APPLICANT: ASAKAWA, Makoto
; APPLICANT: HASEGAWA, Mamoru
; APPLICANT: IIDA, Akihiro
; APPLICANT: HIRATA, Takahiro
; APPLICANT: INOUE, Makoto
; TITLE OF INVENTION: PARAMYXOVIRUS-DERIVED RNP
; FILE REFERENCE: 50026/029001
; CURRENT FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: US/09/966,930
; PRIOR FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: PCT/JP00/03194
; PRIOR FILING DATE: 2000-05-18
; PRIOR APPLICATION NUMBER: JP 2001/283451
; PRIOR FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: JP 11/200740
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 43
; LENGTH: 47
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificially Synthesized Sequence
US-09-966-930-43

Query Match
Best Local Similarity 100.0%; Score 10; DB 9; Length 47;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTTCACCT 10
DB 11 CTTTCACCT 10
```

DB 13 CTTTCACCT 4

RESULT 9  
US-09-966-930-44; Sequence 44, Application US/09966930  
; Publication No. US20030022376A1  
; GENERAL INFORMATION:

; APPLICANT: KITAZATO, Kaio

; APPLICANT: SHU, Tsugumine

; APPLICANT: KUMA, Hidekazu

; APPLICANT: UEDA, Yasuji

; APPLICANT: ASAKAWA, Makoto

; APPLICANT: HASEGAWA, Mamoru

; APPLICANT: IIDA, Akihito

; APPLICANT: HIRATA, Takahiro

; APPLICANT: INOUE, Makoto

; TITLE OF INVENTION: PARAMYXOVIRUS-DERIVED RNP

; FILE REFERENCE: 50026/029001

; CURRENT APPLICATION NUMBER: US/09/966,930

; PRIOR FILING DATE: 2001-09-27

; PRIOR APPLICATION NUMBER: PCT/JP00/03194

; PRIOR FILING DATE: 2000-05-18

; PRIOR APPLICATION NUMBER: JP 2001/283451

; PRIOR FILING DATE: 2001-09-18

; PRIOR APPLICATION NUMBER: JP 11/200740

; NUMBER OF SEQ ID NOS: 64

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 44

; LENGTH: 47

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Artificially Synthesized Sequence

US-09-966-930-44

Query Match  
Best Local Similarity 100.0%; Score 10; DB 9; Length 47;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;OY 1 CTTTCACCT 10  
DB 35 CTTTCACCT 44RESULT 10  
US-09-823-699-10; Sequence 10, Application US/09823699  
; Patent No. US20020002143A1  
; GENERAL INFORMATION:

; APPLICANT: Kano, Munehide

; APPLICANT: Matano, Tetsuro

; APPLICANT: Kato, Atsushi

; APPLICANT: Nagai, Yoshiyuki

; APPLICANT: Hasegawa, Mamoru

; TITLE OF INVENTION: AIDS Virus Vaccines Using Sendai Virus

; FILE REFERENCE: 50026/022002

; CURRENT APPLICATION NUMBER: US/09/823,699

; CURRENT FILING DATE: 2001-03-30

; PRIOR APPLICATION NUMBER: US 60/193,127

; PRIOR FILING DATE: 2000-03-30

; NUMBER OF SEQ ID NOS: 18

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 10

; LENGTH: 63

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: artificially synthesized sequence

Query Match  
Best Local Similarity 100.0%; Score 10; DB 10; Length 63;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;OY 1 CTTTCACCT 10  
DB 17 CTTTCACCT 26RESULT 11  
US-09-471-840-2; Sequence 2, Application US/09471840  
; Patent No. US20020081706A1  
; GENERAL INFORMATION:

; APPLICANT: NAGAI, Yoshiyuki

; APPLICANT: KATO, Atsushi

; APPLICANT: MURAI, Fukashi

; APPLICANT: ASAKAWA, Makoto

; APPLICANT: SAKATA, Tsuneaki

; APPLICANT: HASEGAWA, Mamoru

; APPLICANT: SHIODA, Tatsuo

; TITLE OF INVENTION: Negative Strand RNA Viral Vector Having

; FILE REFERENCE: 50026/004002

; CURRENT APPLICATION NUMBER: US/09/471,840

; PRIOR FILING DATE: 1999-12-23

; PRIOR APPLICATION NUMBER: JP HEI 7-308315

; PRIOR FILING DATE: 1995-10-31

; PRIOR APPLICATION NUMBER: PCT/JP96/03068

; PRIOR FILING DATE: 1996-10-22

; PRIOR APPLICATION NUMBER: 09/070,938

; NUMBER OF SEQ ID NOS: 6

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 2

; LENGTH: 69

; TYPE: DNA

; ORGANISM: Human Immunodeficiency Virus

; FEATURE:

; NAME/KEY: variation

; LOCATION: (35)..(35)

; OTHER INFORMATION: v at 35 is a, c, or g, not t or u.

US-09-471-840-2

Query Match  
Best Local Similarity 100.0%; Score 10; DB 10; Length 69;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;OY 1 CTTTCACCT 10  
DB 17 CTTTCACCT 26RESULT 12  
US-09-471-840-4; Sequence 4, Application US/09471840  
; Patent No. US20020081706A1  
; GENERAL INFORMATION:

; APPLICANT: NAGAI, Yoshiyuki

; APPLICANT: KATO, Atsushi

; APPLICANT: MURAI, Fukashi

; APPLICANT: ASAKAWA, Makoto

; APPLICANT: SAKATA, Tsuneaki

; APPLICANT: HASEGAWA, Mamoru

; APPLICANT: SHIODA, Tatsuo

; TITLE OF INVENTION: Negative Strand RNA Viral Vector Having

; FILE REFERENCE: 50026/004002

; CURRENT APPLICATION NUMBER: US/09/471,840

; CURRENT FILING DATE: 1999-12-23

; PRIOR APPLICATION NUMBER: JP HEI 7-308315

; PRIOR FILING DATE: 1995-10-31

; EARLIER APPLICATION NUMBER: PCT/JP96/03068

EARLIER FILING DATE: 1996-10-22  
EARLIER APPLICATION NUMBER: 09/070,938  
EARLIER FILING DATE: 1998-04-30  
NUMBER OF SEQ ID NOS: 6  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 4  
LENGTH: 69  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Chemical synthesis  
US-09-471-840-4

Query Match  
Best Local Similarity 100.0%; Score 10; DB 10; Length 69;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTTCACCCCT 10  
DB 16 CTTTCACCCCT 25

## RESULT 13

US-09-728-207-2  
Sequence 2, Application US/09728207  
Patent No. US20020098576A1  
GENERAL INFORMATION:  
APPLICANT: NAGAI, Yoshiyuki  
APPLICANT: KATO, Atsushi  
APPLICANT: MURAI, Fukashi  
APPLICANT: SAKATA, Tsuneaki  
APPLICANT: HASEGAWA, Mamoru  
APPLICANT: SHIODA, Tatsuo  
TITLE OF INVENTION: Recombinant Sendai Virus  
FILE REFERENCE: 50026/005001  
CURRENT APPLICATION NUMBER: US/09/728,207  
CURRENT FILING DATE: 2000-12-01  
PRIOR APPLICATION NUMBER: US/09/071,591  
PRIOR FILING DATE: 1998-05-01  
PRIOR APPLICATION NUMBER: JP HEI 7-285417  
PRIOR FILING DATE: 1995-11-01  
PRIOR APPLICATION NUMBER: PCT/JP96/03069  
PRIOR FILING DATE: 1996-10-22  
NUMBER OF SEQ ID NOS: 6  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 2  
LENGTH: 69  
TYPE: DNA  
ORGANISM: Human immunodeficiency virus  
FEATURE:  
NAME/KEY: variation  
LOCATION: (35)...(35)  
OTHER INFORMATION: v at 35 is a, c, or g, not t or u.  
US-09-728-207-2

Query Match  
Best Local Similarity 100.0%; Score 10; DB 10; Length 69;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTTCACCCCT 10  
DB 17 CTTTCACCCCT 26

## RESULT 14

US-09-728-207-4  
Sequence 4, Application US/09728207  
Patent No. US20020098576A1  
GENERAL INFORMATION:  
APPLICANT: NAGAI, Yoshiyuki  
APPLICANT: KATO, Atsushi  
APPLICANT: MURAI, Fukashi  
APPLICANT: SAKATA, Tsuneaki

APPLICANT: HASEGAWA, Mamoru  
APPLICANT: SHIODA, Tatsuo  
TITLE OF INVENTION: Recombinant Sendai Virus  
FILE REFERENCE: 50026/005001  
CURRENT APPLICATION NUMBER: US/09/728,207  
CURRENT FILING DATE: 2000-12-01  
PRIOR APPLICATION NUMBER: US/09/071,591  
PRIOR FILING DATE: 1998-05-01  
PRIOR APPLICATION NUMBER: JP HEI 7-285417  
PRIOR FILING DATE: 1995-11-01  
PRIOR APPLICATION NUMBER: PCT/JP96/03069  
PRIOR FILING DATE: 1996-10-22  
NUMBER OF SEQ ID NOS: 6  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 4  
LENGTH: 69  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Chemical synthesis  
US-09-728-207-4

Query Match  
Best Local Similarity 100.0%; Score 10; DB 10; Length 69;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTTCACCCCT 10  
DB 16 CTTTCACCCCT 25

## RESULT 15

US-09-070-938-2  
Sequence 2, Application US/09070938  
Patent No. US2002010066A1  
GENERAL INFORMATION:  
APPLICANT: Nagai, Yoshiyuki  
APPLICANT: Kato, Atsushi  
APPLICANT: Murai, Fukashi  
APPLICANT: Asakawa, Makoto  
APPLICANT: Sakata, Tsuneaki  
APPLICANT: Hasegawa, Mamoru  
APPLICANT: Shioda, Tatsuo  
TITLE OF INVENTION: Negative Strand RNA Viral  
TITLE OF INVENTION: Vector Having Autonomous Replication Capability  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Clark & Elbing LLP  
STREET: 176 Federal Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02110  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/070,938  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 7-308315  
FILING DATE: 31-OCT-1995  
APPLICATION NUMBER: JP96/03068  
FILING DATE: 22-OCT-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Clark, Paul T  
REGISTRATION NUMBER: 30,162  
REFERENCE/DOCKET NUMBER: 50026/004001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-428-0200

TELEFAX: 617-428-7045  
TELEX:  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 69 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: Other  
US-09-070-938-2

Query Match 100.0%; Score 10; DB 10; Length 69;  
Best Local Similarity 100.0%; Pred. No. 1.9e+03;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CTTTCACCCCT 10  
|||||  
Db 17 CTTTCACCCCT 26

Search completed: March 19, 2003, 02:47:57  
Job time : 51.5 secs



GenCore version 5.1.4.p5\_4578  
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OM nucleic - nucleic search, using sw model

Run on: March 18, 2003, 23:53:50 ; Search time 1320.5 Seconds

(without alignments)  
122.647 Million cell updates/sec

Title: US-09-702-498a-33

Perfect score: 10  
Sequence: 1 CTTTACACCT 10

Scoring table: IDENTITY\_NUC  
Gapop 10.0, Gapept 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

EST:\*  
1: em\_estba:\*  
2: em\_esthum:\*  
3: em\_estin:\*  
4: em\_estnu:\*  
5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_htc:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_htc:\*  
12: gb\_est3:\*  
13: gb\_est4:\*  
14: gb\_est5:\*  
15: em\_estfun:\*  
16: em\_estom:\*  
17: gb\_gss:\*  
18: em\_gss\_hum:\*  
19: em\_gss\_inv:\*  
20: em\_gss\_pln:\*  
21: em\_gss\_vrt:\*  
22: em\_gss\_fun:\*  
23: em\_gss\_mam:\*  
24: em\_gss\_mus:\*  
25: em\_gss\_other:\*  
26: em\_gss\_pro:\*  
27: em\_gss\_rod:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	10	100.0	28 17 TA285H020	AT485473 T. brucei
2	10	100.0	38 17 A2332275	A2332275 IM0060M11
3	10	100.0	43 17 AL754476	AL754476 Arabidops
4	10	100.0	67 17 A2805524	A2805524 2M0066P22
5	10	100.0	68 10 BE138421	BE138421 xrt74904.x
6	10	100.0	72 13 BE1783611	BE1783611 kh35e05.y

C	7	10	100.0	72	17	AZ781553	AZ781553 2M0021103
8	10	100.0	73	17	B36161	B36161 HS-1038-A1-	
9	10	100.0	80	17	FR0032825	FR0032825 Fugu rubr	
10	10	100.0	84	13	B1550671	B1550671 603195845	
11	10	100.0	88	17	BH405910	BH405910 RPCI-23-1	
12	10	100.0	93	17	A2659766	A2659766 IM0537H21	
13	10	100.0	93	17	AG101870	AG101870 Pan trogl	
14	10	100.0	97	9	A1053521	A1053521 q172a01.x	
15	10	100.0	97	9	A1053527	A1053527 q172a08.x	
16	10	100.0	99	17	A2829196	A2829196 2M0106N07	
17	10	100.0	99	17	AQ248921	AQ248921 F18J3-T7.	
C	18	10	100.0	101	13	BJ091421	BJ091421 BJ091421
C	19	10	100.0	102	9	AA731433	AA731433 n294e01.s
C	20	10	100.0	103	13	BI004214	BI004214 MR4-HN005
C	21	10	100.0	103	17	A2519083	A2519083 RPCI-11-2
C	22	10	100.0	107	9	AT000717	AT000717 AT000717
C	23	10	100.0	108	9	AL840443	AL840443 AL840443
24	10	100.0	109	9	AA905844	AA905844 O187d05.s	
C	25	10	100.0	109	10	BB594471	BB594471 BB594471
26	10	100.0	110	10	AM600553	AM600553 707053D02	
27	10	100.0	110	12	BF987980	BF987980 CM0-GN016	
C	28	10	100.0	110	13	BJ537314	BJ537314 B537314
29	10	100.0	110	17	BH809571	BH809571 K07049-3	
30	10	100.0	111	12	BG462159	BG462159 947047B11	
C	31	10	100.0	112	9	A1499089	A1499089 t004e06.x
C	32	10	100.0	112	12	BG604174	BG604174 EST456372
33	10	100.0	112	13	BM191515	BM191515 t487d06.	
34	10	100.0	112	14	W06033	W06033 T9ESTzy80C0	
35	10	100.0	113	12	BF910147	BF910147 CM2-OT008	
C	36	10	100.0	114	13	BI037028	BI037028 CM1-NT020
C	37	10	100.0	115	17	BH088715	BH088715 RPCI-24-9
C	38	10	100.0	116	13	BJ209556	BJ209556 BJ209556
C	39	10	100.0	116	17	TA796312P	TA796312P T. brucei
C	40	10	100.0	117	12	BF992469	BF992469 IL5-GN017
C	41	10	100.0	117	12	AQ385796	AQ385796 RPCI11-14
C	42	10	100.0	117	17	BG794168	BG794168 UTM-SM1C
C	43	10	100.0	119	12	BF604724	BF604724 270864 MA
C	44	10	100.0	120	12	BF174200	BF174200 MYE2738 M
45	10	100.0	121	12	BF174200	BF174200 MYE2738 M	

## ALIGNMENTS

RESULT 1  
TA285H020  
LOCUS  
DEFINITION  
T. brucei sheared genomic DNA clone 285h02, reverse sequence,  
genomic survey sequence.  
ACCESSION  
AL485473  
VERSION  
AL485473.1 GI:11853036  
KEYWORDS  
GSS.  
SOURCE  
Trypanosoma brucei.  
ORGANISM  
Trypanosoma brucei  
Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae;  
Trypanosoma.

REFERENCE  
Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,  
Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,  
Melville, S.E., Rajandream, M.A. and Barrell, B.G.  
TITLE  
Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing  
Project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,  
Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and  
nh@sanger.ac.uk

COMMENT  
Constructed at the Institute for Genomic Research (TIGR),  
Rockville, MD. Genomic DNA isolated from a cloned population of  
Trypanosoma brucei (TRE927/4 GUTat 10.1) was mechanically sheared  
to give a tight size distribution (4 kb). The v + i method used for the library construction is  
described in detail in Smith, H. and Venter, J.C. (Making small  
insert libraries for whole genome shotgun sequencing projects. In  
Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.

Barrell, Oxford University Press, 1999).

Email: nelsayed@tr.org  
Details of T. Bruce sequencing at the Sanger Centre are available  
at [http://www.sanger.ac.uk/Projects/T\\_Bruce/](http://www.sanger.ac.uk/Projects/T_Bruce/).

Location/Qualifiers

1. .28

/organism="Trypanosoma brucei"

/strain="TREU927"

/db\_xref="taxon:5691"

/clone="285h02"

BASE COUNT 5 a 10 c 2 g 11 t

BASE COUNT 10 a 8 c 15 g 5 t

Query Match 100.0%; Score 10; DB 17; Length 28;  
Best Local Similarity 100.0%; Pred. No. 7.8e+04;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 100.0%; Score 10; DB 17; Length 38;  
Best Local Similarity 100.0%; Pred. No. 8.3e+04;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CTTTCACCT 10  
Db 9 CTTTCACCT 18

OY 1 CTTTCACCT 10  
Db 19 CTTTCACCT 10

## RESULT 2

A2332275 38 bp DNA linear GSS 29-SEP-2000

## LOCUS

1H0060M1R mouse 10kb plasmid UUGC1M library Mus musculus genomic

## DEFINITION

Arabidopsis thaliana T-DNA flanking sequence GR-054E08-012357,

## ACCESSION

A2332275

## VERSION

AL754476

## KEYWORDS

A2332275.1 GI:10395775

## KEYWORDS

AL754476.1 GI:21486974

## SOURCE

house mouse.

## SOURCE

GSS.

## ORGANISM

Mus musculus

## ORGANISM

thale cress.

## REFERENCE

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

## REFERENCE

Arabidopsis thaliana

## AUTHORS

Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

## AUTHORS

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

## TITLE

1 (bases 1 to 38)

## TITLE

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

## COMMENT

Mouse whole genome scaffolding with paired end reads from 10kb

## COMMENT

Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

## JOURNAL

Unpublished (2000)

## JOURNAL

Strizhov, N., Li, Y., Rosso, M., Vlehoever, P., Dekker, K., Saedler, H.

## AUTHORS

University of Utah Genome Center

## AUTHORS

and Weisshaar, B.

## COMMENT

plasmid inserts

## COMMENT

A pipeline for automated high-throughput generation of FSTs

## JOURNAL

Unpublished (2000)

## JOURNAL

transfomed lines

## AUTHORS

Contact: Robert B. Weiss

## AUTHORS

2

## COMMENT

University of Utah

## COMMENT

Rosso, M., Li, Y., Strizhov, N. and Weisshaar, B.

## JOURNAL

Km. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT

## JOURNAL

Submitted (17-JUN-2002) Weisshaar B., Max-Planck-Institut fuer

## AUTHORS

84112, USA

## AUTHORS

Zuechtungsforchung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany

## COMMENT

Tel: 801 585 5606

## COMMENT

This sequence is recovered from the left border of the T-DNA. It

## FEATURES

Insert Length: 10000 Std Error: 0.00

## FEATURES

indicates an insertion close to or within gene At3g07160. The

## SOURCE

Seq primer: CACACAGGAAACAGCTATGACC

## SOURCE

sequences are generated at the MPI for Plant Breeding Research in

## CLASS

Class: plasmid ends

## CLASS

the context of the GABI-Kat project. GABI-Kat is part of the German

## High quality sequence stop: 38.

Plant Genomics program designated 'GABI'. Information on line

## High quality sequence stop: 38.

availability can be found at:

## Location/Qualifiers

1. .38

## Location/Qualifiers

<http://www.mpiz-koeln.mpg.de/GABI-Kat/>.

## Location/Qualifiers

/organism="Mus musculus"

## Location/Qualifiers

1. .43

## Location/Qualifiers

/strain="C57BL/6J"

## Location/Qualifiers

/organism="Arabidopsis thaliana"

## Location/Qualifiers

/db\_xref="taxon:10090"

## Location/Qualifiers

/strain="Columbia 0"

## Location/Qualifiers

/clone="UUGC1M0060M1"

## Location/Qualifiers

/db\_xref="taxon:3702"

## Location/Qualifiers

/clone="10kb plasmid UUGC1M library"

## Location/Qualifiers

/clone="GR-054E08-012357"

## Location/Qualifiers

/sex="Male"

## Location/Qualifiers

/note="PCR was performed on DNA from Arabidopsis thaliana

## Location/Qualifiers

/lab-host="E. Coli strain XL10-Gold, T1-resistant, F-"

## Location/Qualifiers

plants (T1) which were transformed with the T-DNA from

## Location/Qualifiers

/note-Vector: PWD42nv; Purified genomic DNA from M.

## Location/Qualifiers

vector pAC161. The lines contain one or more T-DNA

## Location/Qualifiers

musculus C57BL/6J (male) was obtained from the Jackson

## Location/Qualifiers

insertions. The DNA fragment(s) resulting from the PCR

## Location/Qualifiers

Laboratory Mouse DNA Resource

## Location/Qualifiers

were directly sequenced to determine the genomic sequence

## Location/Qualifiers

(<http://www.jax.org/resources/documents/dnares/>). The DNA

## Location/Qualifiers

flanking the insertion. Sequences displaying significant

## Location/Qualifiers

was hydrodynamically sheared by repeated passage through a

## Location/Qualifiers

similarity to the A. thaliana nuclear genome sequence were

## Location/Qualifiers

0.005 inch orifice at constant velocity. The sheared DNA

## Location/Qualifiers

ligated to the blunt ends in high molar excess. The

processed for submission. T-DNA derived sequences were removed

BASE COUNT 8 a 10 c 8 g 17 t

ORIGIN

Query Match 100.0%; Score 10; DB 17; Length 43;  
 Best Local Similarity 100.0%; Pred. No. 8.5e+04;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CTTTCACCT 10  
 |||||  
 Db 33 CTTTCACCT 42

RESULT 4  
 A2805524 67 bp DNA linear GSS 20-FEB-2001  
 LOCUS 2M006P22R Mouse 10kb plasmid UNGC1M library Mus musculus genomic  
 DEFINITION clone UNGC2M006P22 R, DNA sequence.  
 ACCESSION A2805524  
 VERSION A2805524.1 GI:12966335  
 KEYWORDS GSS.  
 SOURCE house mouse.  
 ORGANISM Mus musculus

REFERENCE  
 1. (bases 1 to 67)  
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,  
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,  
 M., Rose, M., Rose, R., Stokes, R., Tinger, A., von Niederhausern, A.,  
 and Wright, D., Weiss, R.

TITLE  
 Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts

JOURNAL  
 COMMENT  
 Contact: Robert B. Weiss  
 University of Utah Genome Center  
 Km. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert length: 10000 Std Error: 0.00  
 Plate: 0066 row: P column: 22  
 Seq primer: CACACAGAAACAGCTATGACC  
 Class: plasmid ends  
 High quality sequence stop: 67.  
 Location/Qualifiers

# FEATURES

1. 67  
 /organism="Mus musculus"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UNG2M006P22"  
 /clone\_11b="Mouse 10kb plasmid UNGC1M library"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (g114732114[95]AF19072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into

chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 23 a 13 c 17 g 14 t

ORIGIN

Query Match 100.0%; Score 10; DB 17; Length 67;  
 Best Local Similarity 100.0%; Pred. No. 9.4e+04;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CTTTCACCT 10  
 |||||  
 Db 34 CTTTCACCT 25

RESULT 5  
 BE138421 68 bp mRNA linear EST 21-JUN-200  
 LOCUS x174904.x2 NCI\_CGAP\_OV26 Homo sapiens CDNA IMAGE:2765910 3',  
 DEFINITION mRNA sequence.  
 ACCESSION BE138421  
 VERSION BE138421.1 GI:8600921  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens

REFERENCE  
 1. (bases 1 to 68)  
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index  
 Unpublished (1997)  
 Contact: Robert Strausberg, Ph.D.  
 Email: cgaps-remail.nih.gov  
 Tissue Procurement: Monica Brown, M.D., Elise Kohn, M.D., Michael  
 R. Emert-Buck, M.D., Ph.D.  
 CDNA Library Preparation: David B. Krizman, Ph.D.  
 CDNA Library Arrayed by: Greg Lennon, Ph.D.  
 DNA sequencing by: Washington University Genome Sequencing Center  
 Clone distribution: NCI-CGAP clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL, send email to:  
 info@image.llnl.gov  
 Possible reversed clone: polyT not found  
 Seq primer: -400P from GIBCO.  
 Location/Qualifiers

# FEATURES

1. 68  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:2765910"  
 /clone\_11b="NCI\_CGAP\_OV26"  
 /sex="female"  
 /tissue\_type="papillary serous carcinoma"  
 /dev\_stage="adult"  
 /lab\_host="DH10B"  
 /note="Organ: ovary; Vector: pAMP1; mRNA made from papillary serous ovarian carcinoma, CDNA made by oligo-dT priming. Directionally cloned. Size-selected on agarose gel, average insert size 500 bp. Primary library, non-amplified."

BASE COUNT 26 a 8 c 22 g 12 t

ORIGIN

Query Match 100.0%; Score 10; DB 10; Length 68;  
 Best Local Similarity 100.0%; Pred. No. 9.4e+04;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CTTTCACCT 10  
 |||||  
 Db 57 CTTTCACCT 48

RESULT 6  
 LOCUS BE1783611 72 bp mRNA linear EST 26-SEP-2001

DEFINITION kh35e05.y1 Ascaris suum male head PAMPI v2 Chiapelli McCarter

ACCESSION B1783611

VERSION B1783611.1 GI:15786503

KEYWORDS EST.

SOURCE plg roundworm.

ORGANISM Ascaris suum

REFERENCE Eukaryota; Metazoa; Nematoda; Chromadorea; Ascarididae; Ascaridoidea 1 (bases 1 to 72)

AUTHORS McCarter, J., Clifton, S., Chiapelli, B., Pape, D., Martin, J., Wylie, T., Dante, M., Maria, M., Hillier, L., Kucaba, T., Thelasing, B., Bowers, Y., Gibbons, M., Ritter, E., Bennett, J., Franklin, C., Tsagarelshvili, R., Ronko, I., Kennedy, S., Maguire, L., Beck, C., Underwood, K., Steptoe, M., Allen, M., Person, B., Swaller, T., Harvey, N., Schurk, R., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.

TITLE The Washington Univ. Nematode EST Project, 1999

JOURNAL Unpublished (1999)

COMMENT Contact: McCarter JP  
The Washington Univ. Nematode EST Project, 1999  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@watson.wustl.edu

The library was constructed by Brandi Chiapelli and Dr. James McCarter at Washington University, St. Louis. The cDNA was made by using Dynabead oligo-dT priming (Dyna). PCR based library using a modified protocol from the SMART PCR cDNA Synthesis Kit from Clontech. Directionally cloned into the UDG sites of PAMPI. Dissected nematode tissues were provided by Dr. Alan Scott (ascotte@hshp.edu) at John Hopkins University in Baltimore, MD. Seq primer: -40RP from Gibco

High quality sequence stop: 58.

Location/Qualifiers

1. 72

/organism="Ascaris suum"

/db\_xref="taxon:6253"

/clone\_lib="Ascaris suum male head PAMPI v2 Chiapelli McCarter"

/sex="Male"

/tissue\_type="Head"

/dev\_stage="Adult"

/lab\_host="DH10B"

/note="Vector: PAMPI (Gibco); Site\_1: NotI; Site\_2: SalI; The library was constructed by Brandi Chiapelli and Dr. James McCarter at Washington University, St. Louis. The cDNA was made by using Dynabead oligo-dT priming (Dyna). PCR based library using a modified protocol from the SMART PCR cDNA Synthesis Kit from Clontech. Directionally cloned into the UDG sites of PAMPI. Dissected nematode tissues were provided by Dr. Alan Scott (ascotte@hshp.edu) at the School of Public Hygiene and Public Health at John Hopkins University in Baltimore, MD."

BASE COUNT 10 a 22 c 15 g 25 t

ORIGIN

Query Match 100.0%; Score 10; DB 13; Length 72;

Best Local Similarity 100.0%; Pred. No. 9.5e+04;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTTCACCT 10

DB 26 CTTTCACCT 35

RESULT 7

AZ781553 72 bp DNA linear GSS 16-FEB-2001

LOCUS 2M0021103F Mouse 10kb plasmid UUGC1M library Mus musculus genomic

DEFINITION clone UUGC2M0021103 F. DNA sequence.

ACCESSION AZ781553

VERSION AZ781553.1 GI:12914361

KEYWORDS GSS.

SOURCE house mouse.

ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 72)

AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C., Islam, H., Longacre, S., Mahmood, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D. Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SIC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0021 row: 1 column: 03  
Seq primer: CCGTGTAAACGCGCCAGT  
Class: plasmid ends

High quality sequence stop: 72.

Location/Qualifiers

1. 72

/organism="Mus musculus"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="UUGC2M0021103"

/clone\_lib="Mouse 10kb plasmid UUGC1M library"

/sex="Male"

/lab\_host="E. coli strain XL10-Gold, TI-resistant, F-"

/note="Vector: PMD42ny; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adapter oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g11473211419b/AF128072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 5 a 26 c 3 g 38 t

ORIGIN

Query Match 100.0%; Score 10; DB 17; Length 72;

Best Local Similarity 100.0%; Pred. No. 9.5e+04;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTTCACCT 10

DB 34 CTTTCACCT 43

RESULT 8

B36161C 73 bp DNA linear GSS 17-OCT-1997

LOCUS HS-1038-A1-E11-MF.ab1 CIT Human Genomic Sperm Library C Homo

DEFINITION sapiens genomic clone Plate-Ct 820 Col-21 Row-I, DNA sequence.

ACCESSION B36161 GI:2535330  
 VERSION B36161.1  
 KEYWORDS GSS.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euthelia; Primates; Catarrhini; Homnidae; Homo.  
 1 (bases 1 to 73)  
 REFERENCE Mahairas,G.G., Zackrone,K.D., Smith,T., Tipton,S., Schmidt,S., Tricoff,R., Abajian,C., Blanchard,A., West,A. and Hood,L.E.  
 Construction of a Characterized Clone Resource for Genomic Sequencing: Generation and Preliminary Analysis of 20,000 Sequence Tagged Connectors  
 Unpublished (1997)  
 CONTACT: Mahairas GG, Zackrone KD, Hood L  
 University of Washington  
 Seattle, WA 98195, USA  
 Tel: (206) 616-8744  
 Fax: (206) 685-7301  
 Email: kzackrone@u.washington.edu  
 Sequence Tagged Connector  
 Plate: CT 820 row: I column: 21  
 Class: BAC ends  
 High quality sequence stop: 73.  
 Location/Qualifiers  
 1. 73  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone="Plate-CT 820 Col-21 Row-I"  
 /clone\_1lb="CIT Human Genomic Sperm Library C"  
 /sex="M"  
 /note="Organ: sperm; Vector: pBelobAC11; BAC Clones in E-Coli DH10B"  
 E-Coli DH10B"

BASE COUNT 21 a 14 c 21 g 16 t 1 others  
 ORIGIN  
 Query Match 100.0%; Score 10; DB 17; Length 73;  
 Best Local Similarity 100.0%; Pred. No. 9.6e+04;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CTTTCACCT 10  
 |||||  
 Db 28 CTTTCACCT 19

RESULT 9  
 FR0032825 80 bp DNA linear GSS 27-JUN-1998  
 LOCUS Fugu rubripes GSS sequence, clone 152F05aG3, genomic survey  
 DEFINITION  
 sequence.  
 ACCESSION AT029193  
 VERSION AT029193.1 GI:3271307  
 KEYWORDS GSS; genome survey sequence.  
 SOURCE Takifugu rubripes.  
 ORGANISM Takifugu rubripes  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes; Tetraodontidae; Takifugu.  
 1 (bases 1 to 80)  
 REFERENCE Elgar,G., Clark,M., Smith,S., Meek,S., Warner,S., Umrانيا,Y., Williams,G. and Brenner,S.  
 Direct Submission  
 Submitted (09-JUN-1998) MRC Human Genome Mapping Project Resource Centre, Hinxton, Cambridge, CB10 1SB, UK. Email: biohelp@hmp.mrc.ac.uk  
 Vector: pBluescript II KS  
 V-type: plasmid  
 PRIMER: KS  
 DESCR: One pass dye-terminator sequencing of cosmid cloned genomic sequence.  
 Location/Qualifiers

source 1. 80  
 /organism="Takifugu rubripes"  
 /db\_xref="taxon:31033"  
 /clone="152F05aG3"  
 /clone\_1lb="cosmid 152F05"  
 BASE COUNT 7 a 22 c 13 g 35 t 3 others  
 ORIGIN  
 Query Match 100.0%; Score 10; DB 17; Length 80;  
 Best Local Similarity 100.0%; Pred. No. 9.7e+04;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0.

OY 1 CTTTCACCT 10  
 |||||  
 Db 39 CTTTCACCT 48

RESULT 10  
 B1550671 84 bp mRNA linear EST 05-SEP-2003  
 LOCUS 603195845F1 NIH\_MGC\_95 Homo sapiens CDNA clone IMAGE:5275475 5', mRNA sequence.  
 DEFINITION  
 mRNA sequence.  
 ACCESSION B1550671  
 VERSION B1550671.1 GI:15437983  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euthelia; Primates; Catarrhini; Homnidae; Homo.  
 1 (bases 1 to 84)  
 REFERENCE NIH-MGC http://mgi.nci.nih.gov/  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cgabs-remail.nih.gov  
 Tissue Procurement: Miklos Palkovits, M.D., Ph.D.  
 CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki Toshiyuki and Piero Carninci (RIKEN)  
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLN at:  
 http://image.llnl.gov  
 Plate: LAM11695 row: 1 column: 12  
 High quality sequence stop: 84.  
 Location/Qualifiers  
 1. 84  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:5275475"  
 /clone\_1lb="NIH\_MGC\_95"  
 /tissue="type="hippocampus"  
 /lab\_host="DH10B"  
 /note="Organ: brain; Vector: pBluescript (modified pBluescript KS+); Site: 1: BamHI; Site: 2: SalI-XhoI (gtcgac); Oligo-dT primed using primer 5'-TTTTTTTTTTTTVN-3', size-selected for average insert size 2.5 kb and normalized to R0T 5. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIH/NHGRI, National Institutes of Health). Note: this is a NIH-MGC Library."

BASE COUNT 19 a 19 c 30 g 16 t  
 ORIGIN  
 Query Match 100.0%; Score 10; DB 13; Length 84;  
 Best Local Similarity 100.0%; Pred. No. 9.6e+04;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0.

OY 1 CTTTCACCT 10  
 |||||  
 Db 21 CTTTCACCT 30

RESULT 11  
BH405910 88 bp DNA linear GSS 19-APR-2002  
LOCUS  
DEFINITION RPCI-23-105F8.SP6E RPCI-23 Mus musculus genomic clone RPCI-23-105F8  
, DNA sequence.  
ACCESSION BH405910  
VERSION BH405910.1 GI:17460796  
KEYWORDS  
SOURCE house mouse.  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 88)  
AUTHORS Young,J.M., Friedman,C., Williams,E.M., Ross,J.A., Tonnes-Priddy,L.  
and Trask,B.J.  
TITLE Different evolutionary processes shaped the mouse and human  
olfactory receptor gene families  
JOURNAL Hum. Mol. Genet. 11 (5), 535-546 (2002)  
MEDLINE 21864068  
COMMENT Contact: Young JM  
Barbara Trask, Division of Human Biology  
Fred Hutchinson Cancer Research Center  
1100 Fairview Avenue N., C3-168, P.O. Box 19024, Seattle, WA  
98109-1024, USA.  
Tel: 206 667 1471  
Fax: 206 667 6524  
Email: jayoung@herc.org  
Young,J.M., Swartzell,S., Friedman,C., Tonnes-Priddy,L., Lane,R.P.,  
Wallace,J.C., Mahairas,G.G., Hood,L., and Trask,B.J. End sequences  
of mouse BACs containing olfactory receptor genes. Unpublished  
Plate: 105 row: F column: 8  
Seq primer: SP6E  
Class: BAC ends.  
Location/Qualifiers

FEATURES  
Source  
1. 88  
/organism="Mus musculus"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="RPCI-23-105F8"  
/clone\_1lb="RPCI-23"  
/sex="Female"  
/lab\_host="DH10B"  
/note="Organ: Kidney/Brain; Vector: pBac3.6; Site\_1:  
EcoRI; Site\_2: EcoRI; Female C57BL/6J mouse kidney and/or  
brain genomic DNA was isolated and partially digested  
with a combination of EcoRI and EcoRI Methylase. Size  
selected DNA was cloned into the pBac3.6 vector at the  
EcoRI sites. The ligation products were transformed into  
DH10B electrocompetent cells (BRL Life Technologies)."  
BASE COUNT 19 a 34 c 11 g 24 t  
ORIGIN

Query Match 100.0%; Score 10; DB 17; Length 88;  
Best Local Similarity 100.0%; Pred. No. 9.9e+04;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CTTTCACCT 10  
|||||  
Db 77 CTTTCACCT 86

RESULT 12  
A2659766 93 bp DNA linear GSS 14-DEC-2000  
LOCUS  
DEFINITION 1M0537H21F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0537H21 F, DNA sequence.  
ACCESSION A2659766  
VERSION A2659766.1 GI:11796912  
KEYWORDS GSS.  
SOURCE house mouse.  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE  
AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 93)  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamll,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly  
M., Rose,M., Rose,R., Stokes,R., Tingy,A., von Niederhausern,A.  
and Wright,D., Weis,R.  
TITLE Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weis  
University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert length: 10000 Std Error: 0.00  
Plate: 0537 row: H column: 21  
Seq primer: CGTTGTAAACGACGCCACT  
Class: plasmid ends  
High quality sequence stop: 93.  
Location/Qualifiers

FEATURES  
Source  
1. 93  
/organism="Mus musculus"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0537H21"  
/clone\_1lb="Mouse 10kb plasmid UUGC1M library"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, TI-resistant, F-"  
/note="Vector: FMD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adapted DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pM42 (g1147321149b1A129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adapted mouse DNA was annealed to  
adapted vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."  
BASE COUNT 17 a 30 c 20 g 26 t  
ORIGIN

Query Match 100.0%; Score 10; DB 17; Length 93;  
Best Local Similarity 100.0%; Pred. No. 1e+05;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CTTTCACCT 10  
|||||  
Db 9 CTTTCACCT 18

RESULT 13  
AG101870 93 bp DNA linear GSS 03-NOV-2001  
LOCUS  
DEFINITION Pan troglodytes DNA, clone: PTB-105A03.R, genomic survey sequence.  
ACCESSION AG101870  
VERSION AG101870.1 GI:16722387  
KEYWORDS GSS.  
SOURCE Pan troglodytes male lymphoblast DNA, clone\_1lb:PTB Chimpanzee Male  
BAC library clone:PTB-105A03.R.  
ORGANISM Pan troglodytes  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE 1 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.  
 AUTHORS Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,  
 Totoki, Y., Watanabe, H. and Sakaki, Y.  
 TITLE BAC end sequences of library PTB  
 JOURNAL Unpublished  
 REFERENCE 2 (bases 1 to 93)  
 AUTHORS Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,  
 Totoki, Y., Watanabe, H. and Sakaki, Y.  
 TITLE Direct Submission  
 JOURNAL Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical  
 and Chemical Research (RIKEN), Genomic Sciences Center (GSC);  
 1-7-22 Suenhiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan  
 (E-mail: chimpesegsc.riken.go.jp, URL: http://hgp.gsc.riken.go.jp/  
 Tel: 81-45-503-9111, Fax: 81-45-503-9170)  
 Clones are derived from the chimpanzee BAC library PTB This BAC end  
 was generated during the R&D process and may have higher chance of  
 clone tracking errors.  
 COMMENT PRIMERS  
 Sequencing: M13Rev  
 LIBRARY  
 Vector : pKS145  
 R Site 1 : SacI  
 R Site 2 : SacI  
 Location/Qualifiers  
 1. 93  
 /organism="Pan troglodytes"  
 /db\_xref="taxon:9598"  
 /clone="PTB-105A03.R"  
 /sex="male"  
 /cell-type="lymphoblast"  
 /clone\_lib="PTB Chimpanzee Male BAC Library"  
 BASE COUNT 11 a 34 c 8 g 34 t 6 others  
 ORIGIN  
 Query Match 100.0%; Score 10; DB 17; Length 93;  
 Best Local Similarity 100.0%; Pred. No. 1e+05;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 CTTTCACCT 10  
 |||||  
 Db 45 CTTTCACCT 54  
 RESULT 14  
 A1053521 97 bp mRNA linear EST 15-JUL-1998  
 LOCUS q172a01.x1 NCI\_CGAP\_OV26 Homo sapiens CDNA clone IMAGE:1861992 3'  
 DEFINITION mRNA sequence.  
 A1053521  
 VERSION A1053521.1 GI:3321308  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE 1 (bases 1 to 97)  
 AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index  
 JOURNAL Unpublished (1997)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs-remail.nih.gov  
 Tissue Procurement: Monica Brown, M.D., Elise Kohn, M.D., Michael  
 R. Emmert-Buck, M.D., Ph.D.  
 CDNA Library Preparation: David B. Kitzman, Ph.D.  
 CDNA Library Arrayed by: Greg Lennon, Ph.D.  
 DNA Sequencing by: Washington University Genome Sequencing Center  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 www-bio.llnl.gov/bdip/image/image.html  
 Seq primer: -40m13 fwd. ET from Amersham.  
 Location/Qualifiers  
 FEATURES  
 SOURCE  
 1. 97  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:1861992"  
 /clone\_lib="NCI\_CGAP\_OV26"  
 /sex="female"  
 /tissue-type="papillary serous carcinoma"  
 /dev\_stage="adult"  
 /lab\_host="DH10B"  
 /note="Organ: ovary; Vector: PAMPI; mRNA made from  
 papillary serous ovarian carcinoma, CDNA made by oligo-dT  
 priming. Directionally cloned. Size-selected on agarose  
 gel, average insert size 500 bp. Primary library,  
 non-amplified."  
 BASE COUNT 14 a 25 c 11 g 47 t  
 ORIGIN  
 Query Match 100.0%; Score 10; DB 9; Length 97;  
 Best Local Similarity 100.0%; Pred. No. 1e+05;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 CTTTCACCT 10  
 |||||  
 Db 32 CTTTCACCT 41

REFERENCE 15  
 A1053527 97 bp mRNA linear EST 15-JUL-1998  
 LOCUS q172a08.x1 NCI\_CGAP\_OV26 Homo sapiens CDNA clone IMAGE:1862006 3'  
 DEFINITION mRNA sequence.  
 A1053527  
 VERSION A1053527.1 GI:3321314  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE 1 (bases 1 to 97)  
 AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index  
 JOURNAL Unpublished (1997)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs-remail.nih.gov  
 Tissue Procurement: Monica Brown, M.D., Elise Kohn, M.D., Michael  
 R. Emmert-Buck, M.D., Ph.D.  
 CDNA Library Preparation: David B. Kitzman, Ph.D.  
 CDNA Library Arrayed by: Greg Lennon, Ph.D.  
 DNA Sequencing by: Washington University Genome Sequencing Center  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 www-bio.llnl.gov/bdip/image/image.html  
 Seq primer: -40m13 fwd. ET from Amersham.  
 Location/Qualifiers  
 FEATURES  
 SOURCE  
 1. 97  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:1862006"  
 /clone\_lib="NCI\_CGAP\_OV26"  
 /sex="female"  
 /tissue-type="papillary serous carcinoma"  
 /dev\_stage="adult"  
 /lab\_host="DH10B"  
 /note="Organ: ovary; Vector: PAMPI; mRNA made from  
 papillary serous ovarian carcinoma, CDNA made by oligo-dT  
 priming. Directionally cloned. Size-selected on agarose  
 gel, average insert size 500 bp. Primary library,  
 non-amplified."  
 BASE COUNT 14 a 25 c 12 g 46 t  
 ORIGIN  
 Query Match 100.0%; Score 10; DB 9; Length 97;  
 Best Local Similarity 100.0%; Pred. No. 1e+05;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 CTTTCACCT 10  
 |||||  
 Db 32 CTTTCACCT 41

Best Local Similarity 100.0%; Pred. No. 1e+05;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTTCACCC 10  
|||||  
Db 31 CTTTCACCC 40

Search completed: March 19, 2003, 01:24:57  
Job time : 1328.5 secs

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